

STIC-Biotech/ChemLib

55886

From: Davis, Minh-Tam
Sent: Monday, December 03, 2001 9:51 AM
To: STIC-Biotech/ChemLib
Subject: RE: Search request for 09/583848

Please use the grandparent cases 08/967727 or 08/037230.
Thanks

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Wednesday, November 21, 2001 11:57 AM
To: Davis, Minh-Tam
Subject: RE: Search request for 09/583848

Unfortunately the Parent Case has no CRF either.

Thank you.

-----Original Message-----

From: Davis, Minh-Tam
Sent: Wednesday, November 21, 2001 11:22 AM
To: STIC-Biotech/ChemLib
Subject: RE: Search request for 09/583848

Please note that in the request, I asked to use the parent case 09/404026 to search for this case.
Tam

-----Original Message-----

From: STIC-Biotech/ChemLib
Sent: Wednesday, November 21, 2001 11:21 AM
To: Davis, Minh-Tam
Subject: RE: Search request for 09/583848

We are unable to process this search because there is a problem with the CRF data for this case. If there is a related case that should be used, please let us know. **We cannot process this request until valid data is available.** Please contact STIC/Biotech.

Biotech/Chem STIC
308-4478

-----Original Message-----

From: Davis, Minh-Tam
Sent: Wednesday, November 21, 2001 10:35 AM
To: STIC-Biotech/ChemLib
Subject: Search request for 09/583848

Please search in commercial database and in issued patent files:

1) SEQ ID NO:18.

2) Please search against the parent cases PCT/US92/04354, 07/807043, 07/764364, 07/728838, 07/705702 for priority date determination.

Please use the parent case 09/404026 to search for this case.

RECEIVED
DEC - 3 2001
(STIC)

error in continuity
file not in biotech
no CRF
5342774

Searcher: D. Schuerber
Phone: 308-4292
Location: CM1 12C14
Date Picked Up: _____
Date Completed: 12/10
Searcher Prep/Review: 8
Clerical: _____
Online time: 16

TYPE OF SEARCH:

NA Sequences: 3
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: Compugen IgFastDB
WWW/Internet: _____
Other (specify): _____

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Thank you
MINH TAM DAVIS
ART UNIT 1642, ROOM 8A01, MB 8E12
305-2008

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 4, 2001, 07:46:17 ; Search time 1159.37 Seconds
(without alignments)
2085.443 Million cell updates/sec

Title: US-08-037-230D-18

Perfect score: 225

Sequence: 1 TATTTCCTTCTGTGATCTT.....CGGACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST.*
- 1: em_estfun.*
 - 2: em_esthum.*
 - 3: em_estin.*
 - 4: em_estom.*
 - 5: em_estpl.*
 - 6: em_estba.*
 - 7: em_estro.*
 - 8: em_estov.*
 - 9: em_hic.*
 - 10: gb_est1.*
 - 11: gb_est2.*
 - 12: gb_hic.*
 - 13: gb_gss.*
 - 14: em_gss_fun.*
 - 15: em_gss_hum.*
 - 16: em_gss_inv.*
 - 17: em_gss_pln.*
 - 18: em_gss_pro.*
 - 19: em_gss_rtd.*
 - 20: em_gss_vrt.*
 - 21: em_gss_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	220.2	97.9	563	11	BG477228
2	220.2	97.9	776	11	BG476912
3	220.2	97.9	876	11	BG792356
4	220.2	97.9	878	11	BG397171
5	220.2	97.9	886	11	BG476078
6	213.8	95.0	623	11	BG793889
7	213.8	95.0	686	11	BG575715
8	213.8	95.0	704	11	B1090658
9	213.8	95.0	769	11	BG765526
10	202.6	90.0	934	11	BG280738
11	201.4	89.5	795	10	BE541476
12	196.8	87.5	590	11	BE897495

13	196.8	87.5	680	10	BE563063
14	196.4	87.3	768	11	BI086876
15	196	87.1	767	11	BI092532
16	195.2	86.8	1089	11	BG029985
17	194	86.2	707	11	BG760839
18	193.6	86.0	484	11	BF970108
19	193.6	86.0	784	11	BF793468
20	178.8	79.5	845	11	BG481937
21	176.8	78.6	894	11	BG765817
22	165.4	73.5	810	10	AL526639
23	164.6	73.2	816	11	BI086919
24	163.4	72.6	797	11	BI087493
25	162.8	72.4	929	11	BE896896
26	159.6	70.9	962	11	BG116297
27	159.6	70.9	1050	11	BG024106
28	156.4	69.5	956	11	BE900736
29	154.8	68.8	876	11	BE795782
30	153.2	68.1	929	10	BE275276
31	152.8	67.9	704	11	BG764972
32	150.2	66.8	845	11	BI089076
33	147.6	65.6	922	11	BG115115
34	147.6	65.6	946	11	BF983819
35	146	64.9	948	10	AL562721
36	141.8	63.0	820	11	BG481340
37	138.6	61.6	1109	11	BG333682
38	138.2	61.4	597	10	BE281072
39	134.2	59.6	828	11	BG479591
40	133.8	59.5	981	10	BE731771
41	131.2	58.3	822	11	BE898065
42	130.8	58.1	950	10	BE541026
43	129.2	57.4	833	11	BG768688
44	127.2	56.5	821	11	BG177776
45	126.8	56.4	538	11	BF241891

ALIGNMENTS

RESULT	1
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LOCUS	BG477228 563 bp mRNA EST 21-MAR-2001
DEFINITION	602524237F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642641 5', mRNA sequence.
ACCESSION	BG477228
VERSION	BG477228.1 GI:13409507
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/BTP CDNA Library Prepared by: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LNCM411 row: i column: 10 High quality sequence stop: 499.
FEATURES	Location/Qualifiers
source	1..563 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4642641" /issue_lib="NIH_MGC_20" /issue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." BASE COUNT 133 a 147 c 162 g 121 t

ORIGIN

Query Match 97.9%; Score 220.2; DB 11; Length 563;
Best Local Similarity 98.7%; Pred. No. 1.2e-47;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCTTTCTGTCATCTTCAGCAAGCTTCGGATTCTTCCTTGCAGCTGGTCTTTGGGCATC 60
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Db 191 TACTTCTTTCTGTCATCTTCAGCAAGCTTCGGATTCTTCCTTGCAGCTGGTCTTTGGGCATC 250
|||
QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
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Db 251 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 310
|||
QY 121 TCCTACGATGGCTCTGCTGGTGACCAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
|||
Db 311 TCCTACGATGGCTCTGCTGGTGACCAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 370
|||

QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 371 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 415
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RESULT 2
BF792356 876 bp mRNA EST 21-MAR-2001
LOCUS 602524881F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4642868 5',
DEFINITION mRNA sequence.

ACCESSION BG476912
VERSION BG476912.1 GI:13409178
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 776)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1412 row: b column: 21
High quality sequence stop: 747.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4642868"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in

FEATURES
source
1..776
Location/Qualifiers
1..776
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in

the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." BASE COUNT 180 a 197 c 232 g 167 t

ORIGIN

Query Match 97.9%; Score 220.2; DB 11; Length 776;
Best Local Similarity 98.7%; Pred. No. 1.3e-47;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCTTTCTGTCATCTTCAGCAAGCTTCGGATTCTTCCTTGCAGCTGGTCTTTGGGCATC 60
|||
Db 191 TACTTCTTTCTGTCATCTTCAGCAAGCTTCGGATTCTTCCTTGCAGCTGGTCTTTGGGCATC 250
|||
QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
|||
Db 251 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 310
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Db 311 TCCTACGATGGCTCTGCTGGTGACCAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 370
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QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||
Db 371 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 415
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RESULT 3
BF792356 876 bp mRNA EST 12-JAN-2001
LOCUS 602252896F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4345222 5',
DEFINITION mRNA sequence.

ACCESSION BF792356
VERSION BF792356.1 GI:12097410
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 876)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM9964 row: p column: 23
High quality sequence stop: 780.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4345222"
/clone_lib="NIH_MGC_84"
/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

FEATURES
source
1..876
Location/Qualifiers
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/organism="Homo sapiens"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 185 a 215 c 248 g 228 t

ORIGIN

Query Match 97.9%; Score 220.2; DB 11; Length 876;

Db	190	TACTTCTTCTGTGATCTTTCAGCAAAAGCTTCCGATTCCTTTCAGCTGGTCTTTGGCATC	249
Qy	61	GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTCTGGGCCTC	120
Db	250	GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTCTGGGCCTC	309
Qy	121	TCCTACGATGCCTGCTGGGTGACAATCAGATCATGCCAGSACAGGCTTCTTGATAATC	180
Db	310	TCCTACGATGCCTGCTGGGTGACAATCAGATCATGCCAGSACAGGCTTCTTGATAATC	369
Qy	181	ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG	225
Db	370	ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTTGAGGAG	414
RESULT 5			
LOCUS	BG476078	886 bp	mRNA
DEFINITION	602520963F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4639670 5',	EST	21-MAR-2001
ACCESSION	BG476078	mRNA sequence.	
VERSION	BG476078.1	GI:13408357	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-re@mail.nih.gov		
	Tissue Procurement: ATCC/DCTD/DRP		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LNCMI403 row: m column: 15		
	High quality sequence stop: 730.		
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	/tissue_type="melanotic melanoma"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site:2:		
	EcoRI; cDNA made by oligo-dT priming. Directionally		
	cloned into EcoRI/XhoI sites using the following 5'		
	adaptor: GGCACGAG(G). Size-selected >500bp for average		
	insert size 1.8kb. Library constructed by Ling Hong in		
	the laboratory of Gerald M. Rubin (University of		
	California, Berkeley) using ZAP-cDNA synthesis kit		
	(Stratagene) and Superscript II RT (Life Technologies)."		
BASE COUNT	183 a 231 c 262 g 210 t		
ORIGIN			
Query Match	97.9%	Score 220.2;	DB 11; Length 886;
Best Local Similarity	98.7%	Pred. No. 1.3e-47;	
Matches 22;	Conservative	0; Mismatches	3; Indels 0; Gaps 0;
Qy	1	TATTTCCTTCTGTGATCTTTCAGCAAAAGCTTCCGATTCCTTTCAGCTGGTCTTTGGCATC	60
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Qy	61	GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTCTGGGCCTC	120
Db	154	GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTCTGGGCCTC	213

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QY 121 TCCTACGATGGCTCTCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCTTGATAATC 180
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Db 214 TCCTACGATGGCTCTCTGGGTGACAAATCAGATCATGCCAGACAGGCTTCTTGATAATC 273
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QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 274 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 318
|||||

RESULT 6
LOCUS BF793889 623 bp mRNA EST 12-JAN-2001
DEFINITION 60225285F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4347380 5',
mRNA sequence.
ACCESSION BF793889
VERSION BF793889.1 GI:12098943
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 623)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9970 row: j column: 21
High quality sequence stop: 622.
Location/Qualifiers
1. 623
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/lab_host="DH10B (phage-resistant)"
/notes="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 136 a 173 c 177 g 137 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 11; Length 623;
Best Local Similarity 96.9%; Pred. No. 5.7e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 326 TATTTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGGTCTTTGGCATC 385
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QY 61 GAGCTGATGGAAGTGAGCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 120
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Db 386 GAGCTGATGGAAGTGAGCCCATCGGCCACTTGTACATCTTTGCCACCTGCCTGGGCCTC 445
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QY 121 TCCTACCATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCTTGATAATC 180
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Db 446 TCCTACCATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCTTGATAATC 505
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QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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RESULT 7
LOCUS BG575715 686 bp mRNA EST 10-APR-2001
DEFINITION 602598794F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4707599 5',
mRNA sequence.
ACCESSION BG575715
VERSION BG575715.1 GI:13583368
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 686)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM10577 row: k column: 24
High quality sequence stop: 682.
Location/Qualifiers
1. 686
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4707599"
/clone_lib="NIH_MGC_87"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: breast; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 148 a 176 c 209 g 153 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 11; Length 686;
Best Local Similarity 96.9%; Pred. No. 5.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGGTCTTTGGCATC 60
|||||
Db 60 TATTTCTTTCTGTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGGTCTTTGGCATC 119
|||||

QY 61 GAGCTGATGGAAGTGAGCCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 120
|||||
Db 120 GAGCTGATGGAAGTGAGCCCATCGGCCACTTGTACATCTTTGCCACCTGCCTGGGCCTC 179
|||||

QY 121 TCCTACCATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCTTGATAATC 180
|||||
Db 180 TCCTACCATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCTTGATAATC 239
|||||

QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 240 GTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 284
|||||

RESULT 8
LOCUS BI090658 704 bp mRNA EST 20-JUN-2001
DEFINITION 602853894F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4995238 5',
mRNA sequence.
ACCESSION BI090658
```


VERSION KEYWORDS SOURCE	BI090658.1 GI:14508988 EST. human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 704)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Prepared by: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1018 row: 1 column: 23 High quality sequence stop: 703.
FEATURES	Location/Qualifiers
source	1..704 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4995238" /clone_lib="NIH_MGC_10" /cell_line="MGC36" /lab_host="DH10B" /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
BASE COUNT	158 a 174 c 214 g 157 t 1 others
ORIGIN	
Query Match	95.0%; Score 213.8; DB 11; Length 704;
Best Local Similarity	96.9%; Pred. No. 5.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
QY 1	TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTGAGCTGGTCTTTGGCATC 60
Db 154	TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTGAGCTGGTCTTTGGCATC 213
QY 61	GAGCTGATGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 214	GAGCTGATGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 273
QY 121	TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTTGATATTC 180
Db 274	TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTTGATATTC 333
QY 181	ATCCTGGCCATAATCGCAAGAGGGCGGACTGTGCCCTCGAGGAG 225
Db 334	GTCTGGCCATAATCGCAAGAGGGCGGACTGTGCCCTCGAGGAG 378
RESULT 9	
BG765526	
LOCUS	BG765526 769 bp mRNA EST 15-MAY-2001
DEFINITION	602739439F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869321 5', mRNA sequence.
ACCESSION	BG765526
VERSION	BG765526.1 GI:14076179
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 769)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Prepared by: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1018 row: 1 column: 23 High quality sequence stop: 703.
FEATURES	Location/Qualifiers
source	1..704 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4995238" /clone_lib="NIH_MGC_10" /cell_line="MGC36" /lab_host="DH10B" /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
BASE COUNT	158 a 174 c 214 g 157 t 1 others
ORIGIN	
Query Match	95.0%; Score 213.8; DB 11; Length 704;
Best Local Similarity	96.9%; Pred. No. 5.8e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
QY 1	TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTGAGCTGGTCTTTGGCATC 60
Db 154	TATTTCTTCTGTGATCTTCAGAAAGCTTCGATTCCTTGAGCTGGTCTTTGGCATC 213
QY 61	GAGCTGATGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 214	GAGCTGATGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 273
QY 121	TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTTGATATTC 180
Db 274	TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTTGATATTC 333
QY 181	ATCCTGGCCATAATCGCAAGAGGGCGGACTGTGCCCTCGAGGAG 225
Db 334	GTCTGGCCATAATCGCAAGAGGGCGGACTGTGCCCTCGAGGAG 378
RESULT 9	
BG765526	
LOCUS	BG765526 769 bp mRNA EST 15-MAY-2001
DEFINITION	602739439F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869321 5', mRNA sequence.
ACCESSION	BG765526
VERSION	BG765526.1 GI:14076179
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 769)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Prepared by: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1018 row: 1 column: 23 High quality sequence stop: 703.
FEATURES	Location/Qualifiers
source	1..769 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4869321" /clone_lib="NIH_MGC_49" /lab_host="DH10B (phage-resistant)" /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT	161 a 218 c 222 g 168 t
ORIGIN	
Query Match	95.0%; Score 213.8; DB 11; Length 769;
Best Local Similarity	96.9%; Pred. No. 5.9e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
QY 1	TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGACAGTGGTCTTTGGCATC 60
Db 374	TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGACAGTGGTCTTTGGCATC 433
QY 61	GAGCTGATGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 434	GAGCTGATGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 493
QY 121	TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTTGATATTC 180
Db 494	TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTTGATATTC 553
QY 181	ATCCTGGCCATAATCGCAAGAGGGCGGACTGTGCCCTCGAGGAG 225
Db 554	GTCTGGCCATAATCGCAAGAGGGCGGACTGTGCCCTCGAGGAG 598
RESULT 10	
BG280738	
LOCUS	BG280738 934 bp mRNA EST 21-FEB-2001
DEFINITION	602401029F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4543566 5', mRNA sequence.
ACCESSION	BG280738
VERSION	BG280738.1 GI:13029662
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 934)
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Prepared by: Life Technologies, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1740 row: n column: 10 High quality sequence stop: 769.
FEATURES	Location/Qualifiers
source	1..769 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4869321" /clone_lib="NIH_MGC_49" /lab_host="DH10B (phage-resistant)" /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT	161 a 218 c 222 g 168 t
ORIGIN	
Query Match	95.0%; Score 213.8; DB 11; Length 769;
Best Local Similarity	96.9%; Pred. No. 5.9e-46;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
QY 1	TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGACAGTGGTCTTTGGCATC 60
Db 374	TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTGACAGTGGTCTTTGGCATC 433
QY 61	GAGCTGATGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 434	GAGCTGATGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 493
QY 121	TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTTGATATTC 180
Db 494	TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCTTGATATTC 553
QY 181	ATCCTGGCCATAATCGCAAGAGGGCGGACTGTGCCCTCGAGGAG 225
Db 554	GTCTGGCCATAATCGCAAGAGGGCGGACTGTGCCCTCGAGGAG 598

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LICM1225 row: i column: 07
 High quality sequence stop: 673.

FEATURES

source
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 /organism="Homo sapiens"
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 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCAGGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 235 a 266 c 267 g 166 t
 ORIGIN

Query Match 90.0%; Score 202.6; DB 11; Length 934;
 Best Local Similarity 95.9%; Pred. No. 5e-43; Indels 0; Gaps 0;
 Matches 208; Conservative 0; Mismatches 9;
 QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATC 60
 Db 418 TATTTCTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATC 477
 QY 61 GAGCTGATGGAAGTGGACCCATCGGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 120
 Db 478 GAGCTGATGGAAGTGGACCCATCGGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTC 537
 QY 121 TCCTACGATGGCTCTGGGTGACATCAGATCATGCCAGCAGGCTTCTCTGATAATC 180
 Db 538 TCCTACGATGGCTCTGGGTGACATCAGATCATGCCAGCAGGCTTCTCTGATAATC 597
 QY 181 APTCTGGCCATAATCCGAAGAGAGGGCGACTGTGCC 217
 Db 598 GTCTGGCCATAATCCGAAGAGAGGGCGACTGTGCC 634

RESULT 11
 BE541476
 LOCUS BE541476 795 bp mRNA EST 09-AUG-2000
 DEFINITION 601067928F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3454135 5',
 mRNA sequence.
 ACCESSION BE541476
 VERSION BE541476.1 GI:9770121
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 795)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LIAM8438 row: h column: 08
 High quality sequence stop: 662.

FEATURES

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 /db_xref="taxon:9606"
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 /clone_lib="NIH_MGC_10"
 /cell_line="MGC36"
 /lab_host="DH10B"
 /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5 kb. Library prepared by Life
 Technologies."

BASE COUNT 182 a 199 c 234 g 180 t
 ORIGIN

Query Match 89.5%; Score 201.4; DB 10; Length 795;
 Best Local Similarity 96.9%; Pred. No. 1e-42; Indels 1; Gaps 1;
 Matches 216; Conservative 0; Mismatches 6;

QY 3 TTCTTTCTCTGTATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATCGA 62
 Db 189 TTCTTTCTCTGTATCTTCAGCAAGCTTCGGATTCCTTGCAGCTGGTCTTTGGCATCGA 247
 QY 63 GCTGATGGAAGTGGACCCATCGGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTCTC 122
 Db 248 GCTGATGGAAGTGGACCCATCGGCCACGCTGTACATCTTTGCCACCTGCTGGGCCTCTC 307
 QY 123 CTAGATGGCTCTGGTGGTACATCAGATCATGCCAGGACAGCTTCTCTGATAATCAT 182
 Db 308 CTAGATGGCTCTGGTGGTACATCAGATCATGCCAGGACAGCTTCTCTGATAATCAT 367
 QY 183 CCTGSCCATATCCGAGAGAGGGCGACTGTGCCCTCGAGGAG 225
 Db 368 CCTGSCCATATCCGAGAGAGGGCGACTGTGCCCTCGAGGAG 410

RESULT 12
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 LOCUS BE897495 590 bp mRNA EST 20-OCT-2000
 DEFINITION 601432326F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3917503 5',
 mRNA sequence.
 ACCESSION BE897495
 VERSION BE897495.1 GI:10363014
 KEYWORDS EST.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 590)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DRP
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LIAM9744 row: c column: 08
 High quality sequence stop: 589.

FEATURES

source
 1. 590
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:3917503"
 /clone_lib="NIH_MGC_72"
 /tissue_type="melanotic melanoma"

Db 538 TACTTCTTCTGTGATCTTCAGCAAGCTTCGGATTCCCTGGAGCTGGTCTTTGGCATC 597
QY 61 GAGCTGATGAAGTGAGCCCATCGGCCAGGTGACATCTTTGCCACCTGCTGGGCTC 120
Db 598 GAGCTGATGAAGTGAGCCCATCGGCCAGGTGACATCTTTGCCACCTGCTGGGCTC 657
QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
Db 658 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 717
QY 181 ATCTGTGCCAT-ATCCGACAGAGGGGAGTGTGCC 217
Db 718 ATCTGTGCATAATCGCAAAAGAGGGGAGTGTGCC 755

RESULT 15
BI092532 767 bp mRNA EST 20-JUN-2001
LOCUS 602857089F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:4998070 5',
DEFINITION mRNA sequence.
ACCESSION BI092532
VERSION BI092532.1 GI:14510862
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 767)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM1026 row: b column: 23
High quality sequence stop: 643.
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1. .767
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4998070"
/clone_11b="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: cervix; Vector: pCMV-SPORT6; Site1: NotI;
Site2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.5 kb. Library prepared by Life
Technologies."

BASE COUNT 164 a 227 c 224 g 152 t
ORIGIN

Query Match 87.1%; Score 196; DB 11; Length 767;
Best Local Similarity 95.1%; Pred. No. 2.6e-41;
Matches 213; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 1 TATTTCCTTCTGTGATCTTCAGCAAGCTTCGGATTCCCTGGAGCTGGTCTTTGGCATC 60
Db 434 TATTTCCTTCTGTGATCTTCAGCAAGCTTCGGATTCCCTGGAGCTGGTCTTTGGCATC 493
QY 61 GAGCTGATGAAGTGAGCCCATCGGCCAGGTGACATCTTTGCCACCTGCTGGGCTC 120
Db 494 GAGCTGATGAAGTGAGCCCATCGGCCAGGTGACATCTTTGCCACCTGCTGGGCTC 553
QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180

Db 554 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 613
QY 181 ATCTGTGCCAT-ATCCGACAGAGGGGAGTGTGCC 223
Db 614 GTCTGTGCCAT-ATCCGACAGAGGGGAGTGTGCC 657

Search completed: December 4, 2001, 11:54:44
Job time: 14907 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2001, 11:00:37 ; Search time 37.69 Seconds
(without alignments)
1352.018 Million cell updates/sec

Title: US-08-037-230D-18
Perfect score: 225
Sequence: 1 TATTCTTCTGTGTGATCTT.....CGGACTGTGCGCTGAGGAG 225

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	225	100.0	225	1	US-07-807-043B-15
2	225	100.0	225	1	US-08-299-849B-18
3	225	100.0	225	2	US-08-142-368A-18
4	225	100.0	225	3	US-08-967-727-18
5	225	100.0	225	4	US-08-037-230D-18
6	220.2	97.9	945	4	US-09-056-105-7
7	220.2	97.9	1019	4	US-09-056-105-13
8	220.2	97.9	1375	2	US-08-993-738A-2
9	220.2	97.9	1375	4	US-08-713-354C-2
10	213.8	95.0	1640	1	US-07-807-043B-11
11	213.8	95.0	1640	1	US-08-299-849B-11
12	213.8	95.0	1640	2	US-08-142-368A-11
13	213.8	95.0	1640	3	US-08-967-727-11
14	213.8	95.0	1640	4	US-08-037-230D-11
15	213.8	95.0	4204	2	US-08-928-615-1
16	213.8	95.0	4204	4	US-09-056-105-6
17	213.8	95.0	4204	4	US-09-166-448-1
18	195.2	86.8	4157	1	US-07-807-043B-9
19	195.2	86.8	4157	1	US-08-299-849B-9
20	195.2	86.8	4157	2	US-08-142-368A-9
21	195.2	86.8	4157	3	US-08-967-727-9
22	195.2	86.8	4157	4	US-08-037-230D-9
23	195.2	86.8	4559	4	US-09-056-105-5
24	163.2	72.5	1084	2	US-08-184-009-110
25	163.2	72.5	1084	2	US-08-458-356-110
26	163.2	72.5	1084	4	US-08-460-736-110
27	163.2	72.5	1094	2	US-08-184-009-109

28	163.2	72.5	1094	2	US-08-458-356-109	Sequence 109, App
29	163.2	72.5	1094	4	US-08-460-736-109	Sequence 109, App
30	163.2	72.5	1691	2	US-08-993-118-8	Sequence 8, Appli
31	163.2	72.5	1691	3	US-08-845-528C-8	Sequence 8, Appli
32	163.2	72.5	2419	1	US-07-807-043B-7	Sequence 7, Appli
33	163.2	72.5	2419	1	US-08-299-849B-7	Sequence 7, Appli
34	163.2	72.5	2419	2	US-08-142-368A-7	Sequence 7, Appli
35	163.2	72.5	2419	3	US-08-967-727-7	Sequence 7, Appli
36	163.2	72.5	2419	4	US-08-037-230D-7	Sequence 7, Appli
37	163.2	72.5	2420	1	US-08-465-167A-23	Sequence 23, Appli
38	163.2	72.5	2420	4	US-09-056-105-4	Sequence 4, Appli
39	163.2	72.5	5674	1	US-07-807-043B-8	Sequence 8, Appli
40	163.2	72.5	5674	1	US-08-190-411A-1	Sequence 1, Appli
41	163.2	72.5	5674	2	US-08-299-849B-8	Sequence 8, Appli
42	163.2	72.5	5674	2	US-08-560-024-1	Sequence 1, Appli
43	163.2	72.5	5674	2	US-08-142-368A-8	Sequence 8, Appli
44	163.2	72.5	5674	3	US-08-967-727-8	Sequence 8, Appli
45	163.2	72.5	5674	4	US-08-037-230D-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-07-807-043B-15
; Sequence 15, Application US/07807043B
; Patent No.. 5342774
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/807,043B
; FILING DATE: 19911212
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-May-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5342774man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 253.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: singular
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: MAGE-6 gene
US-07-807-043B-15

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Query Match      100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGGTCTTTGGCATC 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGGTCTTTGGCATC 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTGGGCTC 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTGGGCTC 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCTGATAATC 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCTGATAATC 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 ATCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
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RESULT 2
US-08-299-849B-18
; Sequence 18, Application US/08299849B
; Patent No. 5612201
; GENERAL INFORMATION:
; APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
; APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
; APPLICANT: Chomez, Patrick
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
; TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,849B
; FILING DATE: 1-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5612201man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5355
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: MAGE-6 gene
US-08-299-849B-18

Query Match      100.0%; Score 225; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGGTCTTTGGCATC 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGGTCTTTGGCATC 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTGGGCTC 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCTGGGCTC 120
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCTGATAATC 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGCAGAGGCTTCCTGATAATC 180
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 ATCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
US-08-142-368A-18
; Sequence 18, Application US/08142368A
; Patent No. 5925729
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;
; APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
; APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,368A
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
```


APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: MAGE-6 gene
US-08-142-368A-18

Query Match 100.0%; Score 225; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATTTCTTCCGTGATCTTCAGCAAGCTTCGGATTCCCTTCAGCTGCTTTTGGCATC 60
Db 1 TATTTCTTCCGTGATCTTCAGCAAGCTTCGGATTCCCTTCAGCTGCTTTTGGCATC 60
QY 61 GAGCTGATGAAGTGGACCCATCGGCCACGTGTACATCTTGGCCACCTGCGTGGCCCTC 120
Db 61 GAGCTGATGAAGTGGACCCATCGGCCACGTGTACATCTTGGCCACCTGCGTGGCCCTC 120
QY 121 TCCTAGATGGCTGCTGGGTGACATCATCGCCACGTGTACATCTTGGCCACCTGCGTGGCCCTC 180
Db 121 TCCTAGATGGCTGCTGGGTGACATCATCGCCACGTGTACATCTTGGCCACCTGCGTGGCCCTC 180
QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGGACTGTGCCCTTGAGGAG 225
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGGACTGTGCCCTTGAGGAG 225

RESULT 4
US-08-967-727-18
Sequence 18, Application US/08967727
Patent No. 6025474
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,727
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
CURRENT APPLICATION DATA:

APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,365
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6025474man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: MAGE-6 gene
US-08-967-727-18

Query Match 100.0%; Score 225; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATTTCTTCCGTGATCTTCAGCAAGCTTCGGATTCCCTTCAGCTGCTTTTGGCATC 60
Db 1 TATTTCTTCCGTGATCTTCAGCAAGCTTCGGATTCCCTTCAGCTGCTTTTGGCATC 60
QY 61 GAGCTGATGAAGTGGACCCATCGGCCACGTGTACATCTTGGCCACCTGCGTGGCCCTC 120
Db 61 GAGCTGATGAAGTGGACCCATCGGCCACGTGTACATCTTGGCCACCTGCGTGGCCCTC 120
QY 121 TCCTAGATGGCTGCTGGGTGACATCATCGCCACGTGTACATCTTGGCCACCTGCGTGGCCCTC 180
Db 121 TCCTAGATGGCTGCTGGGTGACATCATCGCCACGTGTACATCTTGGCCACCTGCGTGGCCCTC 180
QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGGACTGTGCCCTTGAGGAG 225
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGGACTGTGCCCTTGAGGAG 225

RESULT 5
US-08-037-230D-18
Sequence 18, Application US/08037230D
Patent No. 6235525
GENERAL INFORMATION:
APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/037, 230D
;; FILING DATE: 26-MARCH-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US92/04354
;; FILING DATE: 22-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/807,043
;; FILING DATE: 12-DECEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/764,364
;; FILING DATE: 23-SEPTEMBER-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/728,838
;; FILING DATE: 9-JULY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/705,702
;; FILING DATE: 23-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 6235525man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5353
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 688-9200
;; TELEFAX: (212) 838-3884
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 225 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: MAGE-6 gene
US-08-037-230D-18

Query Match 100.0%; Score 225; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 4e-62;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TATTTCTTTCTGTGATCTTCAGCAAAAGCTTCGCAATCTTCGACGTGGTCTTTGGCATC 60
Db 1 TATTTCTTTCTGTGATCTTCAGCAAAAGCTTCGCAATCTTCGACGTGGTCTTTGGCATC 60
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCTGGGCCTC 120
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCTGGGCCTC 120
Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGTGCCCCAGACAGGCTTCCTGATAATC 180
Db 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGTGCCCCAGACAGGCTTCCTGATAATC 180
Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACGTGCCCCCTGAGGAG 225
Db 181 ATCTGGCCATAATCGCAAGAGAGGGCGACGTGCCCCCTGAGGAG 225

RESULT 6
US-056-105-7
;; Sequence 7, Application US/09056105
;; Patent No. 6287569
;; GENERAL INFORMATION:
;; APPLICANT: KIPPS, THOMAS J.
;; APPLICANT: WU, YUNQI
;; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
;; FILE REFERENCE: 233/221
;; CURRENT APPLICATION NUMBER: US/09/056,105
;; EARLIER FILING DATE: 1998-04-06
;; EARLIER APPLICATION NUMBER: 60/043,467
;; EARLIER FILING DATE: 1997-04-10
;; NUMBER OF SEQ ID NOS: 35

;; SOFTWARE: FastSEQ for Windows Version 3.0
;; SEQ ID NO 7
;; LENGTH: 945
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-056-105-7

Query Match 97.9%; Score 220.2; DB 4; Length 945;
Best Local Similarity 98.7%; Pred. No. 2.4e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TATTTCTTTCTGTGATCTTCAGCAAAAGCTTCGCAATCTTCGACGTGGTCTTTGGCATC 60
Db 433 tactttcttctgtatcttcagcaaaagcttcagattcttcagctggtcttttggcatc 492
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCTGGGCCTC 120
Db 493 gagctgagtggaagtggaccccatcgccacgtgtacatctttgcccactgctgggcctc 552
Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGTGCCCCAGACAGGCTTCCTGATAATC 180
Db 553 tctacagatggcctgctgggtgacaatcagatcatgccccagacaggtctctctgataatc 612
Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACGTGCCCCCTGAGGAG 225
Db 613 atcctggccataatcgcaaaagaggcgactgtgcccctgaggag 657

RESULT 7
US-09-056-105-13
;; Sequence 13, Application US/09056105
;; Patent No. 6287569
;; GENERAL INFORMATION:
;; APPLICANT: KIPPS, THOMAS J.
;; APPLICANT: WU, YUNQI
;; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
;; FILE REFERENCE: 233/221
;; CURRENT APPLICATION NUMBER: US/09/056,105
;; CURRENT FILING DATE: 1998-04-06
;; EARLIER APPLICATION NUMBER: 60/043,467
;; EARLIER FILING DATE: 1997-04-10
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: FastSEQ for Windows Version 3.0
;; SEQ ID NO 13
;; LENGTH: 1019
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-056-105-13

Query Match 97.9%; Score 220.2; DB 4; Length 1019;
Best Local Similarity 98.7%; Pred. No. 2.5e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 TATTTCTTTCTGTGATCTTCAGCAAAAGCTTCGCAATCTTCGACGTGGTCTTTGGCATC 60
Db 498 tactttcttctgtatcttcagcaaaagcttcagattcttcagctggtcttttggcatc 557
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCTGGGCCTC 120
Db 558 gagctgagtggaagtggaccccatcgccacgtgtacatctttgcccactgctgggcctc 617
Qy 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGTGCCCCAGACAGGCTTCCTGATAATC 180
Db 618 tctacagatggcctgctgggtgacaatcagatcatgccccagacaggtctctctgataatc 677
Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACGTGCCCCCTGAGGAG 225
Db 678 atcctggccataatcgcaaaagaggcgactgtgcccctgaggag 722

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RESULT 8
US-08-993-738A-2
; Sequence 2, Application US/08993738A
; Patent No. 5928938
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePlaan Etienne;
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski L.L.P.
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/993,738A
; FILING DATE: 19-December-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,354
; FILING DATE: 13-September-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5928938man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5460.1 DIV - JEL/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-993-738A-2

Query Match 97.9%; Score 220.2; DB 2; Length 1375;
Best Local Similarity 98.7%; Pred. No. 2.8e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTTCTCTGATCTTCAGCAAGCTTCGCGATTCTTCGAGCTGGTCTTTGGCATC 60
|| |||||
Db 592 TACTTCTTCTCTGATCTTCAGCAAGCTTCGCGATTCTTCGAGCTGGTCTTTGGCATC 651
|| |||||

QY 61 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCTGGGCTC 120
|| |||||
Db 652 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCTGGGCTC 711
|| |||||

QY 121 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
|| |||||
Db 712 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 771
|| |||||

QY 181 ATCTCGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
|| |||||
Db 772 ATCTCGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 816
|| |||||

RESULT 9
US-08-713-354C-2
; Sequence 2, Application US/08713354C
; Patent No. 6265215
; GENERAL INFORMATION:
; APPLICANT: van der Bruggen, Pierre; DePlaan Etienne;
```

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; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Complex With
; TITLE OF INVENTION: HLA-Cw*16 Molecules, and Uses Thereof
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/713,354C
; FILING DATE: 13-September-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6265215man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1375 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-713-354C-2

Query Match 97.9%; Score 220.2; DB 4; Length 1375;
Best Local Similarity 98.7%; Pred. No. 2.8e-60;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTCTTTCTCTGATCTTCAGCAAGCTTCGCGATTCTTCGAGCTGGTCTTTGGCATC 60
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Db 592 TACTTCTTCTCTGATCTTCAGCAAGCTTCGCGATTCTTCGAGCTGGTCTTTGGCATC 651
|| |||||

QY 61 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCTGGGCTC 120
|| |||||
Db 652 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCTGGGCTC 711
|| |||||

QY 121 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
|| |||||
Db 712 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCTGATAATC 771
|| |||||

QY 181 ATCTCGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 772 ATCTCGCCATAATCGCAAGAGGGCGACTGTGCCCTGAGGAG 816
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RESULT 10
US-07-807-043B-11
; Sequence 11, Application US/07807043B
; Patent No. 5342774
; GENERAL INFORMATION:
; APPLICANT: Boon, Thierry, Van den Eynde, Beno t
; TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
; TITLE OF INVENTION: Rejection Antigens and Uses Thereof
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
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COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,043B
FILING DATE: 19911212
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5342774man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 253.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: cDNA MAGE-3
US-07-807-043B-11

Query Match 95.0%; Score 213.8; DB 1; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.1e-56;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 TATTTCCTTCTGTGATCTTCAGCAAAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 60
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Db 604 TATTTCCTTCTGTGATCTTCAGCAAAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 663
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGGCACCTGCCTGGGCTC 120
|||||
Db 664 GAGCTGATGGAAGTGGACCCCATCGGCACCTGTACATCTTTGGCACCTGCCTGGGCTC 723
Qy 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
|||||
Db 724 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 783
Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 784 GTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 828

RESULT 11
US-08-299-849B-11
Sequence 11, Application US/08299849B
Patent No. 5612201
GENERAL INFORMATION:
APPLICANT: De Plaen, Etienne; Boon-Falleur, Thierry;
APPLICANT: Leth, Bernard; Szikora, Jean-Pierre; De Smet, Charles;
APPLICANT: Chomez, Patrick
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful In
TITLE OF INVENTION: Determining Expression Of A Tumor Antigen Precursor
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/299,849B
FILING DATE: 1-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/037,230
FILING DATE: 26-MARCH-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5612201man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5355
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: cDNA MAGE-3
US-08-299-849B-11

Query Match 95.0%; Score 213.8; DB 1; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.1e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 TATTTCCTTCTGTGATCTTCAGCAAAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 60
|||||
Db 604 TATTTCCTTCTGTGATCTTCAGCAAAAGCTTCGATTCCTTGCAGCTGGTCTTTGGCATC 663
Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
|||||
Db 664 GAGCTGATGGAAGTGGACCCCATCGGCACCTGTACATCTTTGCCACCTGCCTGGGCTC 723
Qy 121 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
|||||
Db 724 TCCTACGATGGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 783
Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
|||||
Db 784 GTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 828

RESULT 12
US-08-142-368A-11
Sequence 11, Application US/08142368A
Patent No. 5925729
GENERAL INFORMATION:
APPLICANT: Boon-Falleur, Thierry; Van der Bruggen, Thierry;

APPLICANT: Van den Eynde, Beno t; Van Pel, Aline; De Plaen, Etienne;
APPLICANT: Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,368A
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/04354
FILING DATE: 22-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/807,043
FILING DATE: 12-DECEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-MAY-1991

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5925729man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5253.4-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: CDNA MAGE-3

US-08-142-368A-11

Query Match 95.0%; Score 213.8; DB 2; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.1e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGAGCTGGTCTTTGGCATC 60
Db 604 TATTTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGAGCTGGTCTTTGGCATC 663

QY 61 GAGCTGATGGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCGTGGCCCTC 120
Db 664 GAGCTGATGGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCGTGGCCCTC 723

QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
Db 724 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 783

QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
Db 784 GTCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 828

RESULT 13

US-08-967-727-11

; Sequence 11, Application US/08967727
; Patent No. 6025474
; GENERAL INFORMATION:
; APPLICANT: Gaugler, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,727
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/037,230
; FILING DATE: 26-MARCH-1993
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,365
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6025474man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1640 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDNA MAGE-3
; US-08-967-727-11

Query Match 95.0%; Score 213.8; DB 3; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.1e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGAGCTGGTCTTTGGCATC 60
Db 604 TATTTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGAGCTGGTCTTTGGCATC 663
QY 61 GAGCTGATGGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCGTGGCCCTC 120

Db 664 GAGCTGATGGAAGTGGAGACCCACCTGGCCACCTGTACATCTTTGGCCACCTGCTGGGCTC 723
Qy 121 TCCTACGATGGCTCTGGGTGACAATCAGATCATGCCAGCAGGCTTCTGTGATAATC 180
Db 724 TCCTACGATGGCTCTGGGTGACAATCAGATCATGCCAAGGAGGCTCTGTGATAATC 783
Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
Db 784 GTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 828

RESULT 14
US-08-037-230D-11
; Sequence 11, Application US/08037230D
; Patent No. 6235525
; GENERAL INFORMATION:
; APPLICANT: Gaudier, B atrice; Van den Eynde, Beno t;
; APPLICANT: van der Bruggen, Pierre; Boon-Falleur, Thierry
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Coding For
; TITLE OF INVENTION: Tumor Rejection Antigen Precursor Mage-3 And Uses Thereof
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/037,230D
; FILING DATE: 26-MARCH-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/04354
; FILING DATE: 22-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/807,043
; FILING DATE: 12-DECEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/764,364
; FILING DATE: 23-SEPTEMBER-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,838
; FILING DATE: 9-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/705,702
; FILING DATE: 23-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6235525man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5353
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1640 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA to mRNA
; FEATURE:
; NAME/KEY: CDNA MAGE-3
US-08-037-230D-11

Query Match 95.0%; Score 213.8; DB 4; Length 1640;
Best Local Similarity 96.9%; Pred. No. 3.1e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC 60
Db 604 TATTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC 663
Qy 61 GAGCTGATGGAAGTGGAGCCCATCGGCCACGTGTACATCTTTTGGCACCTGCTGGGCTC 120
Db 664 GAGCTGATGGAAGTGGAGCCCATCGGCCACGTGTACATCTTTTGGCACCTGCTGGGCTC 723
Qy 121 TCCTACGATGGCTCTGGGTGACAATCAGATCATGCCAGCAGGCTTCTGTGATAATC 180
Db 724 TCCTACGATGGCTCTGGGTGACAATCAGATCATGCCAAGGAGGCTCTGTGATAATC 783
Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
Db 784 GTCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 828

RESULT 15
US-08-928-615-1
; Sequence 1, Application US/08928615
; Patent No. 5965535
; GENERAL INFORMATION:
; APPLICANT: Chau, Pascal
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon, Thierry
; APPLICANT: van der Bruggen, Pierre
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED
; TITLE OF INVENTION: BY HLA CLASS II MOLECULES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,615
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: L0461/7017
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2465...3406
US-08-928-615-1

Query Match 95.0%; Score 213.8; DB 2; Length 4204;
Best Local Similarity 96.9%; Pred. No. 4.6e-58;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TATTCTTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCAGCTGGTCTTTGGCATC 60

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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCGCTGGGCTC 120
Db 2957 GAGCTGATGGAAGTGGACCCCATCGGCCACTGTACATCTTTGCCACCTGCGCTGGGCTC 3016
QY 121 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCAGGAGAGGCTTTCCTGATAATC 180
Db 3017 TCCTACGATGGCCTGCTGGGTGACAATCAGATCATGCCAGGAGAGGCTTTCCTGATAATC 3076
QY 181 ATCCTGGCCATAATCGCAAGAGAGGGGAGTGTGCCCTGAGGAG 225
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Job time: 4622 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2001, 11:29:17 ; Search time 98.92 Seconds
(without alignments)
1950.042 Million cell updates/sec

Title: US-08-037-230D-18
Perfect score: 225
Sequence: 1 TATTCTTTCCTGATCTT.....GCGACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	225	100.0	225	13 AAO32362	MAGE-6 gene. Homo
2	225	100.0	225	15 AAO72487	Tumour rejection a
3	225	100.0	225	20 AAX84122	MAGE-6 gene. Homo
4	223.4	99.3	225	16 AAT01166	MAGE-6 gene. Homo
5	220.2	97.9	1362	20 AAX87596	CLYTA-MAGE-3-His f
6	220.2	97.9	1375	19 AAV22716	MAGE-6 cDNA. Homo
7	220.2	97.9	4204	22 AAS02056	DNA encoding molec
8	213.8	95.0	945	22 AAD12993	Human MAGE-A3 DNA.
9	213.8	95.0	1212	20 AAX87592	Haemagglutinin-MAG
10	213.8	95.0	1353	20 AAX87588	Lipoprotein D-MAGE
11	213.8	95.0	1640	15 AAO72480	Tumour rejection a

12	213.8	95.0	1640	20 AAX84116	MAGE-3 gene. Homo
13	213.8	95.0	4204	20 AAX26974	cDNA encoding MAGE
14	213.8	95.0	4204	21 AAA37927	Human MAGE-A3 nucl
15	212.2	94.3	1640	13 AAO32355	MAGE-3 cDNA. Homo
16	195.2	86.8	920	22 AAI24300	Probe #14233 for g
17	195.2	86.8	920	22 AAI49576	Probe #18262 used
18	195.2	86.8	920	22 AAI15118	Probe #5051 for ge
19	195.2	86.8	1956	22 AAI36453	Probe #5139 used t
20	195.2	86.8	4157	13 AAO32353	MAGE-2 gene. Homo
21	195.2	86.8	4157	15 AAO72478	Tumour rejection a
22	195.2	86.8	4157	20 AAX84114	MAGE-2 gene. Homo
23	195.2	86.8	4523	22 AAD06131	Human MAGE-12 gene
24	166	73.8	379	18 AAT63345	Human MAGE-3 cDNA.
25	163.2	72.5	930	22 AAD12987	Human MAGE-A1 cDNA
26	163.2	72.5	1084	15 AAO67866	H6/MAGE-1 expressi
27	163.2	72.5	1084	20 AAZ08442	H6/MAGE-1 expressi
28	163.2	72.5	1094	15 AAO67865	H6/MAGE-1 expressi
29	163.2	72.5	1094	20 AAZ08441	H6/MAGE-1 expressi
30	163.2	72.5	1338	20 AAX87593	CLYTA-MAGE-1-His f
31	163.2	72.5	1341	20 AAX87591	Lipoprotein D-MAGE
32	163.2	72.5	1624	22 AAF24676	Nucleotide sequenc
33	163.2	72.5	1691	20 AAV69719	Tumour rejection a
34	163.2	72.5	2418	20 AAX84103	E antigen precursor
35	163.2	72.5	2419	13 AAO32351	Antigen E gene. H
36	163.2	72.5	2419	15 AAO72476	Tumour rejection a
37	163.2	72.5	2419	16 AAT05086	MZ2-MEL antigen E
38	163.2	72.5	2419	20 AAX84112	Antigen E coding s
39	163.2	72.5	2420	15 AAO72472	Tumour rejection a
40	163.2	72.5	2420	16 AAO85435	Human melanoma ant
41	163.2	72.5	5674	13 AAO32352	MAGE-1 nucleic aci
42	163.2	72.5	5674	15 AAO72477	Tumour rejection a
43	163.2	72.5	5674	20 AAX84113	MAGE-1 gene. Homo
44	163.2	72.5	5724	16 AAO98902	Tumour rejection a
45	159.6	70.9	1022	20 AAX40199	MAGE-4 encoding ge

ALIGNMENTS

RESULT	1
AAQ32362	AAQ32362 standard; DNA; 225 BP.
ID	AAQ32362
XX	AAQ32362;
AC	AAQ32362;
XX	22-APR-1993 (first entry)
DT	22-APR-1993 (first entry)
XX	MAGE-6 gene.
DE	MAGE-6 gene.
XX	Melanoma antigen; MAGE TRA; melanoma antigen tumor rejection antigen;
KW	tumor rejection antigen precursor; MAGE; antigen E; gene family; ss.
XX	Homo sapiens.
OS	Homo sapiens.
XX	WO9220356-A.
PN	26-NOV-1992.
XX	26-NOV-1992.
XX	22-MAY-1992; 92WO-US04354.
XX	23-MAY-1991; 91US-0705702.
PR	09-JUL-1991; 91US-0728838.
PR	23-SEP-1991; 91US-0764364.
PR	12-DEC-1991; 91US-0807043.
XX	(LUDW-) LUDWIG INST CANCER RES.
PA	Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
XX	Van Den Eynde B, Van Der Bruggen P, Van Pel A;
PI	WPI; 1992-415460/50.
XX	Nucleic acid mol. encoding a human tumour rejection antigen
DR	
XX	
PT	

PT precursor - useful as an immunostimulant in a vaccine for
 XX treating and preventing cancers, also useful in diagnosis
 XX
 PS Disclosure; Page 88; 142pp; English.

XX The sequences given in AAQ32352-69 represent a new family of genes
 CC referred to as melanoma antigens (MAGE). The cDNAs of this gene
 CC family were identified during the isolation of the antigen E gene.
 CC The MAGE cDNAs, when tested, did not transfer expression of antigen
 CC E, but they did show substantial homology to the antigen E cDNA
 CC sequence. The MAGE DNAs share a certain degree of homology with each
 CC other and are expressed in tumour cells including several types of
 CC human tumor cells as well as in human tumors. MAGE expression is not
 CC restricted to melanomas. MAGE refers to a family of tumor rejection
 CC antigen precursors. The antigens resulting from these genes are
 CC referred to as MAGE TRANS or melanoma antigen tumor rejection antigens.
 CC See also AAQ32351.

XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 13; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.3e-56;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTTCTGATCTTCAGCAAGCTTCGATTCCTTGACAGCTGGTCTTTGGCATC 60
 DB 1 tattttctcttgatcttcagcaagcttcgattcccttgacagctggtctttggcatc 60
 QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACCTGTACATCTTTTGGCCACTGCCTGGGCTC 120
 DB 61 gagctgatggaagtggaccccatcgccacgtgacatctttggccacctgctgggctc 120
 QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGCTTCCTGATAATC 180
 DB 121 tcctacgatgctgctgggtgacaatcagatcatgccaggacagcttcctgataatc 180
 QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
 DB 181 atctggccataatcgcaagagagggcgactgtgccctgaggag 225

RESULT 2

AAQ72487
 ID AAQ72487 standard; cDNA to mRNA; 225 BP.

XX AC AAQ72487;

XX 22-JUN-1995 (first entry)

XX Tumour rejection antigen MAGE-6 cDNA.

XX Tumour rejection antigen; melanoma antigen-6; MAGE-6; MAGE-3;
 KW cancer; cytolytic T cells; antigen D; human leucocyte antigen;
 KW ss.

XX Homo sapiens.

XX W09423031-A.

XX 13-OCT-1994.

XX 17-MAR-1994; 94WO-US02877.

XX 26-MAR-1993; 93US-0037230.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
 XX WPI; 1994-333192/41.

XX New tumour rejection antigen precursor MAGE3 - useful in

PT treatment and diagnosis of cancer
 XX Example 32; Page 73; 105pp; English.

XX AAQ72487 is the cDNA sequence which codes for melanoma antigen-6
 CC (MAGE-6). Another melanoma antigen MAGE-3 is encoded by
 CC AAQ72470, this is a tumour rejection antigen precursor. Melanomas
 CC characterised by the expression of MAGE-3 can be detected, or
 CC monitored, by contacting a test sample with an agent that can
 CC recognise MAGE-3. The melanoma can be treated by the administration
 CC of cytolytic T cells specific for the complex of antigen D (the
 CC mature rejection antigen derived from MAGE-3) and a human leucocyte
 CC antigen (esp. HLA-A1).

XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;

Query Match 100.0%; Score 225; DB 15; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.3e-56;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCCTTCTGATCTTCAGCAAGCTTCGATTCCTTGACAGCTGGTCTTTGGCATC 60
 DB 1 tattttctcttgatcttcagcaagcttcgattcccttgacagctggtctttggcatc 60
 QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACCTGTACATCTTTTGGCCACTGCCTGGGCTC 120
 DB 61 gagctgatggaagtggaccccatcgccacgtgacatctttggccacctgctgggctc 120
 QY 121 TCCTACGATGCGCTGCTGGGTGACAATCAGATCATGCCAGGACAGCTTCCTGATAATC 180
 DB 121 tcctacgatgctgctgggtgacaatcagatcatgccaggacagcttcctgataatc 180
 QY 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
 DB 181 atctggccataatcgcaagagagggcgactgtgccctgaggag 225

RESULT 3

AAQ84122
 ID AAX84122 standard; cDNA; 225 BP.

XX AC AAX84122;

XX 08-SEP-1999 (first entry)

XX MAGE-6 gene.

XX Tumour rejection antigen; vaccine; cancer; MAGE-6 gene; ss.

XX Homo sapiens.

XX US5925729-A.

XX 20-JUL-1999.

XX 02-MAY-1994; 94US-0142368.

XX 02-MAY-1994; 94US-0142368.

XX 23-MAY-1991; 91US-0705702.

XX 09-JUL-1991; 91US-0728838.

XX 23-SEP-1991; 91US-0764365.

XX 12-DEC-1991; 91US-0807043.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;

XX Van Den Eynde B, Van Der Bruggen P, Van Pel A;

XX WPI; 1999-418294/35.

XX New tumour rejection antigen is useful as a vaccine against
 PT cancerous diseases

XX Disclosure; Column 69-70; 58pp; English.
XX
XX This sequence represents the MAGE-6 gene sequence.
CC The invention relates to a tumour rejection antigen sequence that is
CC useful as a tumour rejection antigen for vaccination against cancerous
CC conditions.
XX
XX Sequence 225 BP; 44 A; 65 C; 58 G; 58 T; 0 other;
SQ

Query Match 100.0%; Score 225; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 3.3e-56;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTCTTCCCTGTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGCTTTGGCANC 60
DB 1 TATTTCTTCCCTGTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGCTTTGGCANC 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGCCCTC 120
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGCCCTC 120
QY 121 TCCTACGATGGCTGCTGGTGACATTCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
DB 121 TCCTACGATGGCTGCTGGTGACATTCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
QY 181 ATCTGCGCATATTCGCAAGAGAGGCGGACTGTGCCCTGAGGAG 225
DB 181 ATCTGCGCATATTCGCAAGAGAGGCGGACTGTGCCCTGAGGAG 225

RESULT 4
AAT01166
ID AAT01166 standard; DNA; 225 BP.
XX
XX AAT01166;
XX
XX 26-FEB-1996 (first entry)
XX
XX MAGE-6 gene.
XX
XX MAGE-6; melanoma; tumour rejection antigen; cancer; diagnosis; ss.
XX
XX Homo sapiens.
XX
XX W09523874-A1.
XX
XX 08-SEP-1995.
XX
XX 23-FEB-1995; 95WO-US02203.
XX
XX 30-NOV-1994; 94US-0346774.
XX
XX 01-MAR-1994; 94US-0204727.
XX
XX 10-MAR-1994; 94US-0209172.
XX
XX 01-SEP-1994; 94US-0299849.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Boon-Falleur T, Brasseur F, Chomez P, De Plaen E;
PI De Smet C, Gaugier B, Lethé B, Marchand M, Patard J;
PI Szikora J, Van Den Bynde B, Van Derbruggen P, Weynants P;
XX
XX WPI; 1995-320586/41.
XX
XX Determn. of cancerous condition(s) - using a nucleic acid as a
PT primer to determine expression of a MAGE tumour rejection antigen
PT precursor
XX
XX Example 32; Page 80; 121pp; English.
XX
XX A family of human tumour rejection antigen precursor, MAGE, genes
CC (AAT05091-99, AAT01165-71) was isolated from various tumour cell lines.

CC cDNA (AAT01166) coding for MAGE-6 was obtd. from human melanoma
CC LB-33-MEL cells. MAGE serve as markers for tumour diagnosis. The
CC genes are silent in normal cells.
XX
XX Sequence 225 BP; 44 A; 56 C; 57 G; 58 T; 0 other;
SQ

Query Match 99.3%; Score 223.4; DB 16; Length 225;
Best Local Similarity 99.6%; Pred. No. 9.8e-56;
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TATTTCTTCCCTGTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGCTTTGGCANC 60
DB 1 TATTTCTTCCCTGTGATCTTCAGCAAGCTTCGGATTCTTCAGCTGCTTTGGCANC 60
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGCCCTC 120
DB 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGCCCTC 120
QY 121 TCCTACGATGGCTGCTGGTGACATTCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
DB 121 TCCTACGATGGCTGCTGGTGACATTCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
QY 181 ATCTGCGCATATTCGCAAGAGAGGCGGACTGTGCCCTGAGGAG 225
DB 181 ATCTGCGCATATTCGCAAGAGAGGCGGACTGTGCCCTGAGGAG 225

RESULT 5
AAX87596
ID AAX87596 standard; cDNA; 1362 BP.
XX
XX AAX87596;
XX
XX 26-OCT-1999 (first entry)
XX
XX CLYTA-MAGE-3-His fusion DNA.
XX
XX MAGE-3; CLYTA-MAGE-3-His; fusion protein; tumour; melanoma;
KW breast cancer; bladder cancer; lung cancer; colon cancer;
KW head and squamous cell carcinoma; oesophagus carcinoma; vaccine;
KW human; ss.
XX
XX Chimeric - Streptococcus pneumoniae.
XX
XX Chimeric - Homo sapiens.
XX
XX Chimeric - synthetic.
XX
XX W09940188-A2.
XX
XX 12-AUG-1999.
XX
XX 02-FEB-1999; 99WO-EP00660.
XX
XX 06-FEB-1998; 98GB-0002650.
XX
XX 05-FEB-1998; 98GB-0002543.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Cabazon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
PI
XX WPI; 1999-494293/41.
XX
XX P-PSDB; AAY06593.
XX
XX New protein derivatives used in cancer vaccine therapy for treating
PT a range of cancers including melanomas, carcinomas and cancers of
PT breast
XX
XX Example 10; Page 72; 72pp; English.
XX
XX This DNA sequence codes for a fusion protein (see AAY06593) composed
CC of the C-terminal portion of the Streptococcus pneumoniae LYTA
CC protein (CLYTA), the human MAGE-3 tumour-associated antigen and a
CC hexahistidine tail. A vector designed for recombinant expression

XX The sequence represents the coding sequence of molecule for disease
CC detection and treatment, mddt21, shown by computer analysis to be similar
CC to the MAGE family of proteins. The sequence may be used for
CC somatic or germline gene therapy. Gene therapy may be performed to:
CC correct genetic deficiency such as in severe combined immunodeficiency
CC syndrome associated with adenosine deaminase (ADA) deficiency, cystic
CC fibrosis, thalassemias, familial hypercholesterolaemia and haemophilia
CC caused by factor VIII or factor IX deficiencies; (ii) express a
CC conditional lethal gene product (such as in the case of cancers which
CC result from unregulated cell proliferation); (iii) express a protein
CC which affords protection against intracellular parasites (for example,
CC human retroviruses such as HIV, hepatitis B or C, fungal parasites such
CC as Candida albicans and Paracoccidioides brasiliensis, and protozoal
CC parasites such as Plasmodium falciparum and Trypanosoma brasiliensis.
XX
SQ Sequence 4204 BP; 947 A; 1145 C; 1219 G; 893 T; 0 other;

Query Match . 97.9%; Score 220.2; DB 22; Length 4204;
Best Local Similarity 98.7%; Pred. No. 2e-54;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 TATTCTTCTCGTGATCTTCAGCAAGCTTCGGATTCCCTGAGCTGGTCTTTGGCATC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2897 tactttctctgtgatcttcagcaagcttcgattccttcgagctggtctttggcatc 2956
QY 61 GAGCTGATGGAAGTGACCCCATCGCCACGTGTACATCTTGGCCACCTGCCCTGGCCCTC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2957 gagctgatggaagtggaccccatcgccacgtgtacatctttgccacctgctgggacctc 3016
QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCCTGATAATC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3017 tctacgatggcctgctgggtgacaatcagatcatcctccaaagacaggtctcctgataatc 3076
QY 181 ATCTCGGCATATCGACAGAGAGGCGACTGTGCCCTCGAGGAG 225
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3077 atctggccataatcgcaaaaggaggcgactgtgccctgaggag 3121

RESULT 8
AADI2993
ID AADI2993 standard; DNA; 945 BP.
XX
AC AAD12993;
XX
DT 16-OCT-2001 (first entry)
XX
DE Human MAGE-A3 DNA.
XX
KW MAGE antigenic peptide; Human leukocyte antigen; HLA-B35; HLA-B44;
KW tumour cell; immunostimulant; antigen presentation; cancer; melanoma;
KW CD8+ cytotoxic T lymphocyte; colorectal; prostate; gastric carcinoma;
KW myeloma; brain tumour; sarcoma; seminoma; ovarian tumour; cytostatic;
KW gene therapy; human; MAGE-A3; tumour rejection antigen; TRA; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..945
FT /*tag= a
FT /product= "MAGE-A3 protein"
XX
XX WO200153833-A1.
XX
PD 26-JUL-2001.
XX
PF 19-JAN-2001; 2001WO-US02008.
XX
XX 20-JAN-2000; 2000US-0177242.
PR 25-OCT-2000; 2000US-0243212.
XX
PA (LUDW-) LUDWIG INST CANCER RES.

XX
PI Luiten R, Boon-Falleur T, Van Der Bruggen P, Stroobant V;
Demotte N, Schultz E;
XX
DR WPI: 2001-488724/53.
DR P-PSDB; AAE06853.
XX
PT Functional variants and isolated mimetics of a MAGE-A1 HLA-B35 or
HLA-B44 binding peptide, or of a MAGE-A3 HLA-B35 binding peptide, used
in diagnosis and treatment of a disorder characterized by expression of
MAGE-A1 or -A3 -
XX
PS Example 3; Page 94-95; 103pp; English.
XX
CC The invention relates to functional variants and isolated mimetics of a
MAGE-A1 human leukocyte antigen (HLA)-B35 or HLA-B44 binding peptide,
or of a MAGE-A3 HLA-B35 binding peptide, identified by methods described
in the specification. MAGE genes encode tumour rejection antigens
(TRAs) presented to T lymphocytes by HLA-B35 and HLA-B44 molecules.
The MAGE antigenic peptide acts by binding to HLA molecules
on tumour cells and stimulating recognition of these cells and thus
signalling them to the immune system for destruction. The peptide when
presented by HLA molecule induces the activation and stimulation of
CD8+ cytotoxic T lymphocytes. The MAGE antigenic peptide is used to
treat and diagnose disorders characterised by expression of MAGE-A1
or -A3. Disorders include cancers e.g melanomas, oesophageal, lung,
head and neck, breast, colorectal, prostate, renal, bladder,
hepatocellular, papillary thyroid and gastric carcinomas, myelomas,
brain tumours, sarcomas, seminomas, and ovarian tumours. The present
sequence is human MAGE-A3 DNA.
XX
SQ Sequence 945 BP; 210 A; 254 C; 278 G; 203 T; 0 other;

Query Match 95.0%; Score 213.8; DB 22; Length 945;
Best Local Similarity 96.9%; Pred. No. 9.2e-53;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 TATTCTTCTCGTGATCTTCAGCAAGCTTCGGATTCCCTGAGCTGGTCTTTGGCATC 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
433 tactttctctgtgatcttcagcaagcttcgattccttcgagctggtctttggcatc 492
QY 61 GAGCTGATGGAAGTGACCCCATCGCCACGTGTACATCTTCCACCTGCCCTGGCCCTC 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
493 gagctgatggaagtggaccccatcgccactgtacatctttgccacctgctgggacctc 552
QY 121 TCCTACGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGGCTTCCCTGATAATC 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
553 tctacgatggcctgctgggtgacaatcagatcatcctccaaagacaggtcctcctgataatc 612
QY 181 ATCTCGGCATATCGCAAGAGAGGCGACTGTGCCCTCGAGGAG 225
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
613 gtctggccataatcgcaaaaggaggcgactgtgccctgaggag 657

RESULT 9
AAX87592
ID AAX87592 standard; cDNA; 1212 BP.
XX
AC AAX87592;
XX
DT 26-OCT-1999 (first entry)
XX
DE Haemagglutinin-MAGE-3-His fusion DNA.
XX
KW MAGE-3; haemagglutinin; NS1-MAGE-3-His; fusion protein; tumour;
KW melanoma; breast cancer; bladder cancer; lung cancer;
KW head and squamous cell carcinoma; colon cancer;
KW oesophagus carcinoma; vaccine; human; ss.
XX
OS Chimeric - Influenza virus.
OS Chimeric - Homo sapiens.
OS Chimeric - synthetic.

```
XX W09940188-A2.
XX
XX
XX
XX 12-AUG-1999.
XX
XX 02-FEB-1999; 99WO-EP00660.
XX
XX 06-FEB-1998; 98GB-0002650.
XX 05-FEB-1998; 98GB-0002543.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Cabazon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX WPI; 1999-494293/41.
XX P-PSDB; AAY06591.
XX
XX New protein derivatives used in cancer vaccine therapy for treating
XX a range of cancers including melanomas, carcinomas and cancers of
XX breast
XX
XX Example 7; Page 69; 72pp; English.
XX
XX This DNA sequence codes for a fusion protein (see AAY06591) composed
XX of haemagglutinin NSI of influenza virus, the human MAGE-3
XX tumour-associated antigen and a hexahistidine tail. A vector
XX designed for recombinant expression of the fusion protein is
XX provided. MAGE-3 cDNA was amplified using primers that altered the
XX first 5 codons to Escherichia coli codon usage. The NSI moiety
XX provided the fusion protein with additional exogenous T-helper
XX epitopes. The invention relates to MAGE proteins fused to an
XX immunological fusion partner, e.g. NSI-MAGE-3-His. These novel
XX fusion proteins provide vaccines for immunotherapy of melanomas or
XX other MAGE-associated tumours like breast, bladder, lung and
XX non-small cell lung cancer, head and squamous cell carcinoma, colon
XX carcinoma and oesophagus carcinoma.
XX
XX Sequence 1212 BP; 289 A; 319 C; 344 G; 260 T; 0 other;

Query Match 95.0%; Score 213.8; DB 20; Length 1212;
Best Local Similarity 96.9%; Pred. No. 1e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGAGTTCCTTGCAGCTGGTCTTTGGGCATC 60
Db 673 tatttcttctgtgatcttcagcaagcttcagcaagcttcagcttcgttcttgggcatac 732

Qy 61 GAGCTGATGGAAGTGGACCCCGCCACGTGTACATCTTTGCCACCTGCTGGGCCCTC 120
Db 733 gagctgatggaagtggaccacctggccacctgtacatctttgccacctgctgggcctc 792

Qy 121 TCCTACGATGCGCTGCTGGTGCACAAATCAGATCATGCGCCAGACAGGCTTCTGTATAATC 180
Db 793 tcctacgatgacctgctgggtgacaatcagatcatgccaaggcaggcctcctgataatc 852

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
Db 853 gtcttggccataatcgcaagagagggcgactgtgcccctgaggag 897

RESULT 10
AAX87588
ID AAX87588 standard; cDNA; 1353 BP.
XX
XX AAX87588;
XX
XX 26-OCT-1999 (first entry)
XX
XX Lipoprotein D-MAGE-3-His fusion DNA.
XX
XX MAGE-3; lipoprotein D; LPD-MAGE-3-His; fusion protein; tumour;
XX melanoma; breast cancer; bladder cancer; lung cancer;
```

```
KW head and squamous cell carcinoma; colon cancer;
KW oesophagus carcinoma; vaccine; human; ss.
XX
XX Chimeric - Haemophilus influenzae.
OS
OS Chimeric - Homo sapiens.
OS
XX W09940188-A2.
XX
XX 12-AUG-1999.
XX
XX 02-FEB-1999; 99WO-EP00660.
XX
XX 06-FEB-1998; 98GB-0002650.
XX 05-FEB-1998; 98GB-0002543.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Cabazon Silva T, Cohen J, Slaoui MM, Vinals Bassols C;
XX WPI; 1999-494293/41.
XX P-PSDB; AAY06589.
XX
XX New protein derivatives used in cancer vaccine therapy for treating
XX a range of cancers including melanomas, carcinomas and cancers of
XX breast
XX
XX Example 1; Page 66; 72pp; English.
XX
XX This DNA sequence codes for a fusion protein (see AAY06589) composed
XX of lipitated protein D (LPD) of Haemophilus influenzae B, the human
XX MAGE-3 tumour-associated antigen and a hexahistidine tail. A
XX vector designed for recombinant expression of the fusion protein is
XX provided. MAGE-3 cDNA was amplified using primers that altered the
XX first 5 codons to Escherichia coli codon usage. The LPD moiety
XX provided the fusion protein with additional exogenous T-cell
XX epitopes and also increased expression levels in E. coli. The
XX lipid tail ensured optimal presentation of the antigen to
XX antigen-presenting cells. The affinity tag facilitated
XX purification. The invention relates to MAGE proteins fused to an
XX immunological fusion partner, e.g. LPD-MAGE-3-His. These novel
XX fusion proteins provide vaccines for immunotherapy of melanomas or
XX other MAGE-associated tumours like breast, bladder, lung and
XX non-small cell lung cancer, head and squamous cell carcinoma, colon
XX carcinoma and oesophagus carcinoma.
XX
XX Sequence 1353 BP; 342 A; 337 C; 354 G; 320 T; 0 other;
```

```
Query Match 95.0%; Score 213.8; DB 20; Length 1353;
Best Local Similarity 96.9%; Pred. No. 1e-52;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGAGTTCCTTGCAGCTGGTCTTTGGGCATC 60
Db 814 tatttcttctgtgatcttcagcaagcttcagcttccttgcagctggtcttgggcatac 873

Qy 61 GAGCTGATGGAAGTGGACCCCGCCACGTGTACATCTTTGCCACCTGCTGGGCCCTC 120
Db 874 gagctgatggaagtggaccacctggccacctgtacatcttggccacctgctgggcctc 933

Qy 121 TCCTACGATGCGCTGCTGGTGCACAAATCAGATCATGCGCCAGACAGGCTTCTGTATAATC 180
Db 934 tcctacgatgacctgctgggtgacaatcagatcatgccaaggcaggcctcctgataatc 993

Qy 181 ATCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
Db 994 gtcttggccataatcgcaagagagggcgactgtgcccctgaggag 1038
```

```
RESULT 11
AAQ72480
ID AAQ72480 standard; cDNA to mRNA; 1640 BP.
```

XX AAQ72480;
 AC 22-JUN-1995 (first entry)
 DT Tumour rejection antigen precursor MAGE-3 cDNA.
 XX
 DE Tumour rejection antigen precursor MAGE-3 cDNA.
 XX
 KW Tumour antigen rejection precursor; melanoma antigen-3; MAGE-3;
 KW cancer; cytolytic T cells; antigen D; human leucocyte antigen;
 KW PIA gene; ss.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FT 172..1116
 FT CDS /*tag= a
 FT
 XX
 PN W09423031-A.
 PD 13-OCT-1994.
 PD
 XX
 PE 17-MAR-1994; 94NO-US02877.
 PE
 XX
 PR 26-MAR-1993; 93US-0037230.
 PR
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Boon-falleur T, Gaugler B, Van DEN EYNDE B, Van DER BRUGGEN P;
 PI WPI; 1994-333192/41.
 DR
 XX
 XX New tumour rejection antigen precursor MAGE3 - useful in
 PT treatment and diagnosis of cancer
 PT
 XX
 XX
 PS Example 32; Page 64; 105pp; English.
 XX
 CC AAQ72480 is the PIA gene fragment which contains the cDNA coding
 CC sequence AAQ72470, which encodes melanoma antigen-3 (MAGE-3), a tumour
 CC rejection antigen precursor. Melanomas characterised by the expression of
 CC MAGE-3 can be detected, or monitored, by contacting a test sample with
 CC an agent that can recognise MAGE-3. The melanoma can be treated by the
 CC administration of cytolytic T cells specific for the complex of
 CC antigen D (the mature rejection antigen derived from MAGE-3) and a
 CC human leucocyte antigen (esp. HLA-A1).
 XX
 SQ Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;
 Query Match 95.0%; Score 213.8; DB 15; Length 1640;
 Best Local Similarity 96.9%; Pred. No. 1.1e-52;
 Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TATTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGGCAGCTGCTTGGCATC 60
 Db 604 tattcttctgtgattctcagaaagcttcaggttccttgcagctggtcttggcattc 663
 QY 61 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCTC 120
 Db 664 gactgatggaagtggaccacctggccacctgtacatctttgccacctgctgggctc 723
 QY 121 TCCTACGATGCGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
 Db 724 tcctacgatggctgctgggtgacaatcagatcatgcccaaggcaggccctcctgataatc 783
 QY 181 ATCTGCGCCATATCGCAAGAGGGGCGACTGTGCCCTGAGGAG 225
 Db 784 gtctggccataatcgcaagagggcgactgtgccctgaggag 828
 RESULT 12
 AAX84116
 ID AAX84116 standard; cDNA to mRNA; 1640 BP.
 DE
 XX

AC AAX84116;
 XX 08-SEP-1999 (first entry)
 DT
 XX MAGE-3 gene.
 DE
 XX Tumour rejection antigen; vaccine; cancer; MAGE-3 gene; ss.
 KW
 XX Homo sapiens.
 OS
 XX US5925729-A.
 PN
 XX 20-JUL-1999.
 PD
 XX 02-MAY-1994; 94US-0142368.
 PF
 XX 02-MAY-1994; 94US-0142368.
 PR 23-MAY-1991; 91US-0705702.
 PR 09-JUL-1991; 91US-0728838.
 PR 23-SEP-1991; 91US-0764365.
 PR 12-DEC-1991; 91US-0807043.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 XX Boon T, Chomez P, De Plaen E, Lurquin C, Traversari C;
 PI Van Den Eynde B, Van Der Bruggen P, Van Pel A;
 XX WPI; 1999-418294/35.
 DR
 XX New tumour rejection antigen is useful as a vaccine against
 PT cancerous diseases
 PT
 XX Disclosure; Column 51-54; 58pp; English.
 PS
 XX This sequence represents the MAGE-3 gene sequence.
 CC The invention relates to a tumour rejection antigen sequence that is
 CC useful as a tumour rejection antigen for vaccination against cancerous
 CC conditions.
 XX
 SQ Sequence 1640 BP; 380 A; 402 C; 457 G; 401 T; 0 other;
 Query Match 95.0%; Score 213.8; DB 20; Length 1640;
 Best Local Similarity 96.9%; Pred. No. 1.1e-52;
 Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 TATTCTTCTGATCTTCAGCAAGCTTCGATTCCTTGGCAGCTGCTTGGCATC 60
 Db 604 tattcttctgtgattctcagaaagcttcaggttccttgcagctggtcttggcattc 663
 QY 61 GAGCTGATGGAAGTGGACCCATCGGCCAGCTGTACATCTTTGCCACCTGCCTGGGCTC 120
 Db 664 gactgatggaagtggaccacctggccacctgtacatctttgccacctgctgggctc 723
 QY 121 TCCTACGATGCGCTGCTGGGTGACAAATCAGATCATGCCAGGACAGGCTTCCTGATAATC 180
 Db 724 tcctacgatggctgctgggtgacaatcagatcatgcccaaggcaggccctcctgataatc 783
 QY 181 ATCTGCGCCATATCGCAAGAGGGGCGACTGTGCCCTGAGGAG 225
 Db 784 gtctggccataatcgcaagagggcgactgtgccctgaggag 828
 RESULT 13
 AAX26974
 ID AAX26974 standard; cDNA; 4204 BP.
 XX
 AC AAX26974;
 XX
 XX 25-JUN-1999 (first entry)
 DT
 XX cDNA encoding MAGE-3 polypeptide.
 DE
 XX

MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: MAGE-6 gene

Initial Score = 225 Optimized Score = 225 Significance = 1.46
Residue Identity = 100% Matches = 225 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
TATTCTTCTGTCGATCTTCAGCAAGCTTCGATTCCTTGGCAGCTGGTCTTGGCATGAGCTGATGAA
|||||
TATTCTTCTGTCGATCTTCAGCAAGCTTCGATTCCTTGGCAGCTGGTCTTGGCATGAGCTGATGAA
X 10 20 30 40 50 60 70
GTGACCCCATCGCCACGCTGATCATCTTGGCCACCTGCTGGCCCTCTCTAGCATGGCTGCTGGTGAC
80 90 100 110 120 130 140
GTGACCCCATCGCCACGCTGATCATCTTGGCCACCTGCTGGCCCTCTCTAGCATGGCTGCTGGTGAC
80 90 100 110 120 130 140
150 160 170 180 190 200 210
AATCAGATCATGCGCCAGCAGGCTTCTGATATCATCTGCGCATATCGCAAGAGGGGAGCTGTGCC
150 160 170 180 190 200 210
AATCAGATCATGCGCCAGCAGGCTTCTGATATCATCTGCGCATATCGCAAGAGGGGAGCTGTGCC
220 X
CCTGAGGAG
|||||
CCTGAGGAG
220 X

2. US-08-037-230D-18 (1-225)
US-07-807-043B-1 Sequence 11, Application US/07807043B

Sequence 11, Application US/07807043B
Patent No. 5342774
GENERAL INFORMATION:
APPLICANT: Boon, Thierry, Van den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigen Precursors, Tumor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,043B
FILING DATE: 19911212
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5342774man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 253.3
TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1640 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
FEATURE:
NAME/KEY: cDNA MAGE-3

Initial Score = 218 Optimized Score = 218 Significance = 1.38
Residue Identity = 96% Matches = 218 Mismatches = 7
Gaps = 0 Conservative Substitutions = 0

AGCCGGTCACAAAGGAGAAATCTCTGGGAGTGTCTCGGAAATTTGGCAGTATTTCTTCTCTGTGATCTTCA
560 570 580 590 600 610 620
X 10 20
TATTCTTCTCTGTGATCTTCA
|||||
GAAAGCTTCCGATTTCTTCCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGCTGT
30 40 50 60 70 80 90
|||||
GAAAGCTTCCGATTTCTTCCAGCTGGTCTTTGGCATCGAGCTGATGGAAGTGGACCCCATCGCCACGCTGT
630 640 650 660 670 680 690
ACATCTTTGCCACCTGCGCTGGGCTCTCTCTACGATGGCTGCTGCAATCAGATCATGATGCGCCAGGACAG
100 110 120 130 140 150 160
ACATCTTTGCCACCTGCGCTGGGCTCTCTCTACGATGGCTGCTGCAATCAGATCATGATGCGCCAGGACAG
700 710 720 730 740 750 760
170 180 190 200 210 220 X
GCTTCTTGATAATCATCTCGCCATATCGCAAGAGAGGGGAGCTGTGCCCTTGAGGAG
|||||
GCTTCTTGATAATCATCTCGCCATATCGCAAGAGAGGGGAGCTGTGCCCTTGAGGAG
770 780 790 800 810 820 830 840
AGCTGAGTGTGTTAGAGGCTTTTTCAGGGGAGGGAAGA
850 860 870

3. US-08-037-230D-18 (1-225)
US-07-807-043B-9 Sequence 9, Application US/07807043B

Sequence 9, Application US/07807043B
Patent No. 5342774
GENERAL INFORMATION:
APPLICANT: Boon, Thierry, Van den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigen Precursors, Tumor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,043B
FILING DATE: 19911212
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838

FILING DATE: 9-JULY-1991
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5342774man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 253.3
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4157 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
FEATURE:
NAME/KEY: MAGE-2 gene

Initial Score = 205 Optimized Score = 206 Significance = 1.23
Residue Identity = 91% Matches = 206 Mismatches = 19
Gaps = 0 Conservative Substitutions = 0

```

          X      10      20
          TATTCTTTCTGTGATCTTCA
          ||||| ||||| ||||| |||||
ACCCGGTCACAAAGCGAGAAATCGTGGAGAGTGCTCTCAGAAATTCGCCAGGACTCTTTCCCGTGATCTCA
2980 2990 3000 3010 3020 3030 3040 3050
          GCAAAGCTTCCGATTCCTTGGCAGCTGTTGGCATCGAGCTGATGGAAGTGGACCCATCGCCACGCTGT
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GCAAGCCTCCGAGTACTTGCAGCTGGTCTTGGATCGAGGTGGTGGAGTGGTCCCATCAGCCACATGT
3060 3070 3080 3090 3100 3110 3120
          100 110 120 130 140 150 160
          ACATCTTCCACCTGCCCTGCGCTCTCTACGATGGCTGCTGGTGACATCAGATCATGCCAGGACAG
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          ACATCTTGTACCTGCGCTGCGCTCTCTACGATGGCTGCTGGTGACATCAGTCTATGCCAAGACAG
          3130 3140 3150 3160 3170 3180 3190
          170 180 190 200 210 220 X
          GCTTCTGATAATCTCTGGCCATAATCGCAAGAGAGGCGACTGTGCCCTCGAGGAG
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          GCTCTGATAATCTCTGGCCATAATCGCAATAGAGGCGACTGTGCCCTGAGGAGAAATCTGGGAGG
          3200 3210 3220 3230 3240 3250 3260
          AGCTGAGTATGTTGGAGGTGTTTGGGGGAGGAGGA
          3270 3280 3290 3300
```

4. US-08-037-230D-18 (1-225)
US-07-807-043B-7 Sequence 7, Application US/07807043B
Patent No. 5342774
GENERAL INFORMATION:
APPLICANT: Boon, Thierry, Van den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/807,043B
FILING DATE: 19911212
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/764,364
FILING DATE: 23-SEPTEMBER-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/728,838
FILING DATE: 9-JULY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705,702
FILING DATE: 23-May-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5342774man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 253.3
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2419 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: singular
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA

Initial Score = 184 Optimized Score = 186 Significance = 0.99
Residue Identity = 82% Matches = 186 Mismatches = 39
Gaps = 0 Conservative Substitutions = 0

```

          X      10      20
          TATTCTTTCTGTGATCTTCA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AGCCGATCAAAAGCGAGAAATGCTGGAGAGTGTCATCAAAAATTACAAGCACTGTTTCTCGAGATCTCG
990 1000 1010 1020 1030 1040 1050
          30 40 50 60 70 80 90
          GCAAAGCTTCCGATTCCTTGGCAGCTGTTGGCATCGAGCTGATGGAAGTGGACCCATCGCCACGCTGT
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          GCAAAGCCTCTGAGTCTTGGCAGCTGTTGGCATCGAGCTGATGGAAGTGGACCCATCGCCACGCTCT
          1060 1070 1080 1090 1100 1110 1120 1130
          100 110 120 130 140 150 160
          ACATCTTGGCACCCTGCGCTCTCTACGATGGCTGCTGGTGACATCAGATCATGCCAGGACAG
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          ATGCTCTTCTACCTGCTAGTGTCTCTATGATGGCTGCTGGTGATTAATCAGATCATGCCAAGACAG
          1140 1150 1160 1170 1180 1190 1200
          170 180 190 200 210 220 X
          GCTTCTGATAATCTCTGGCCATAATCGCAAGAGAGGCGACTGTGCCCTCGAGGAG
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
          GCTTCTGATAATCTCTGGCTGATGTCATGTCATGAGGCGGCCCTCTCTCGAGGAGAAATCTGGGAGG
          1210 1220 1230 1240 1250 1260 1270
          AGCTGAGTGTGAGGAGTGTATGATGGGAGGAGCA
          1280 1290 1300 1310
```

5. US-08-037-230D-18 (1-225)
US-07-807-043B-8 Sequence 8, Application US/07807043B
Patent No. 5342774
GENERAL INFORMATION:
APPLICANT: Boon, Thierry, Van den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch

CTTCAGC--AAAGCTTCCGATTCCCTTGCAGCTGGTCTTTGGCATCGAG-CTGATGGAAGTGGACCCCATCGG

US-07-807-043B-2 Sequence 2, Application US/07807043B

Sequence 2, Application US/07807043B

Patent No. 5342774

GENERAL INFORMATION:

APPLICANT: Boon, Thierry, Van den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/807,043B

FILING DATE: 19911212

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/764,364

FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/728,838

FILING DATE: 9-JULY-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/705,702

FILING DATE: 23-May-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5342774man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 253.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-3884

TELEFAX: (212) 688-9200

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 675 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: singular

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

Initial Score = 24 Optimized Score = 59 Significance = -0.85
Residue Identity = 47% Matches = 71 Mismatches = 63
Gaps = 15 Conservative Substitutions = 0

CTTGCAGCTGGCTTTGGCATGCGAGCTGATGGAAGTGGACCCCATCGGCCAGCTGT-ACATCTTTGGCCACCT
|||||
ATGCTCTGATAAC-AAAGAAACCA
X 10 20

110 120 130 140 150 160 170
GCCTGGGCTTCCTACGATGGCTGTG-GGTGA---CAATCAGATC-ATGCCACAGACAGG--CTTCCT
|||||
GACAAAGCC-CACAGTGGCTCAGGTGGTGACGGTGTGGAATAGGTGCAATTTATTGACCCGGTACTCCCT
30 40 50 60 70 80 90

180 190 200 210 220 X
GATAATCATCTGGCCATA-ATCGCAAGAGAGGGC--GACTGTGCCCTTGAGGAG
|||||
GGAAGAAATTC-T-GCCTTATCTAGGTGGCTGTTCGCTGTGTGCACAAACAGTTTCTGGCGCTCCAGA
100 110 120 130 140 X 150 160

TGTTTCATAGACGCCCTTTATGAGGACGAGTAGT
170 180 190

15. US-08-037-230D-18 (1-225)
US-07-807-043B-3 Sequence 3, Application US/07807043B

Sequence 3, Application US/07807043B

Patent No. 5342774

GENERAL INFORMATION:

APPLICANT: Boon, Thierry, Van den Eynde, Beno t
TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor
TITLE OF INVENTION: Rejection Antigens and Uses Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/807,043B

FILING DATE: 19911212

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/764,364

FILING DATE: 23-SEPTEMBER-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/728,838

FILING DATE: 9-JULY-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/705,702

FILING DATE: 23-May-1991

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5342774man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 253.3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-3884

TELEFAX: (212) 688-9200

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 228 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: singular

TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

Initial Score = 11 Optimized Score = 68 Significance = -1.00
Residue Identity = 44% Matches = 77 Mismatches = 85
Gaps = 12 Conservative Substitutions = 0

10 20 30 40 50 60 70
CTTTCCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATCGAGCTG--ATG-GAAGT
|||||
GCATCGAGTTGCAAGGCCGAGA
X 10 20

80 90 100 110 120 130 140
GGACCCCATCGGCCACGCTGTACATCTTTGCCACCTGCCCTGCGCTCTCTCTAGCATGGCTGCTGGTGACAA
|||||
AGAAAGAAATGGACA-GCGGA-AGAAGTGGTTGTTTTTTTCCCTTCATTAATTTCTAGTTTCTAGTAA
30 40 50 60 70 80 90

150 160 170 180 190 200 210
T-CAGATCATGCCAGGACAGAGCTTCCTGATATCATCTGCGCATATCGCAAGAGAGGCGGCTGTGCC
|||||
TCCAGAAAT----TTGATTTGTT-CTAAAGTTTCAATTAT-GCAAGATGTCACCAACAGACTTCTGACTGC
100 110 120 130 140 150

220 X

CTGAGGAG
||
ATGCTGAACCTTCATATGATACATAGGATTACACTTGTACCTGTGTAAAAATAAAAGTT
160 X 170 180 190 200 210

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2001, 09:45:42 : Search time 1322.08 Seconds
(without alignments)
2807.595 Million cell updates/sec

Title: US-08-037-230D-18

Perfect score: 225

Sequence: 1 TATTTCCTTCCTGTGATCTT.....GCGACTGTGCCCTGAGGAG 225

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_om.*

20: em_or.*

21: em_ov.*

22: em_pat.*

23: em_ph.*

24: em_pl.*

25: em_ro.*

26: em_sts.*

27: em_sy.*

28: em_un.*

29: em_vi.*

30: em_htgo_hum.*

31: em_htgo_inv.*

32: em_htgo_rod.*

33: em_htg_hum.*

34: em_htg_inv.*

35: em_htg_rod.*

36: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	225	100.0	225	6	AR153509	AR153509 Sequence
2	225	100.0	225	6	I36933	I36933 Sequence 18
3	220.2	97.9	945	9	HSU10339	U10339 Human MAGE-
4	220.2	97.9	1019	9	HUMMAGEB	D32076 Human mRNA
5	220.2	97.9	1362	6	AX019384	AX019384 Sequence
6	220.2	97.9	3871	9	HSU10691	U10691 Human MAGE-
7	220.2	97.9	245077	9	AF002997	AF002997 Homo sapi
8	213.8	95.0	1212	6	AX019380	AX019380 Sequence
9	213.8	95.0	1353	6	AX019376	AX019376 Sequence
10	213.8	95.0	1640	6	AR153502	AR153502 Sequence
11	213.8	95.0	1640	6	I36926	I36926 Sequence 11
12	213.8	95.0	1663	9	BC011744	BC011744 Homo sapi
13	213.8	95.0	1709	9	BC000340	BC000340 Homo sapi
14	213.8	95.0	1753	9	BC005963	BC005963 Homo sapi
15	213.8	95.0	4204	6	AR079453	AR079453 Sequence
16	213.8	95.0	4204	9	HSU03735	U03735 Human MAGE-
c 17	213.8	95.0	245077	9	AF002997	AF002997 Homo sapi
c 18	213.8	95.0	289248	9	U82671	U82671 Homo sapien
19	196.8	87.5	1678	9	BC003408	BC003408 Homo sapi
20	195.2	86.8	4157	6	AR153500	AR153500 Sequence
21	195.2	86.8	4157	6	I36924	I36924 Sequence 9
22	195.2	86.8	4523	6	AX119704	AX119704 Sequence
23	195.2	86.8	4523	9	HUMMAGE12X	L18877 Human MAGE-
24	195.2	86.8	4559	9	HUMMAGE2X	L18920 Human MAGE-
25	195.2	86.8	289248	9	U82671	U82671 Homo sapien
c 26	192	85.3	15260	2	AC084372	AC084372 Homo sapi
27	163.2	72.5	1084	6	AR052774	AR052774 Sequence
28	163.2	72.5	1094	6	AR052773	AR052773 Sequence
29	163.2	72.5	1338	6	AX019382	AX019382 Sequence
30	163.2	72.5	1341	6	AX019377	AX019377 Sequence
31	163.2	72.5	1624	6	AX060181	AX060181 Sequence
32	163.2	72.5	2419	6	AR153498	AR153498 Sequence
33	163.2	72.5	2419	6	I36922	I36922 Sequence 7
34	163.2	72.5	2420	6	AR007331	AR007331 Sequence
35	163.2	72.5	2420	9	HUMMAG1A	M77481 Human antig
36	163.2	72.5	5674	6	AR060975	AR060975 Sequence
37	163.2	72.5	5674	6	AR153499	AR153499 Sequence
38	163.2	72.5	5674	6	I24013	I24013 Sequence 1
39	163.2	72.5	5674	6	I36923	I36923 Sequence 8
c 40	163.2	72.5	275159	9	U82670	U82670 Homo sapien
41	159.6	70.9	954	9	HSU10340	U10340 Human MAGE-
42	159.6	70.9	1022	9	HUMMAGEA	D32075 Human mRNA
43	159.6	70.9	1022	9	HUMMAGEC	D32077 Human mRNA
44	159.6	70.9	2531	6	AR153505	AR153505 Sequence
45	159.6	70.9	2531	6	I36929	I36929 Sequence 14

ALIGNMENTS

RESULT 1

AR153509 AR153509 225 bp DNA PAT 08-AUG-2001
LOCUS Sequence 18 from patent US 6235525.
ACCESSION AR153509
VERSION AR153509.1 GI:15121041

KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
AUTHORS 1 (bases 1 to 225)
TITLE van den Eynde,B., van der Bruggen,P. and Boon-Falleur,T.
Isolated nucleic acid molecules coding for tumor rejection antigen precursor MAGE-3 and uses thereof

JOURNAL Patent: US 6235525-A 18 22-MAY-2001;
FEATURES Location/Qualifiers
source 1..225

BASE COUNT 44 a 65 c 58 g 58 t
ORIGIN

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Query Match      100.0%; Score 225; DB 6; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATC 60
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Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATC 60

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCACCTGCCTGGGCTC 120
    |||
Db 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCACCTGCCTGGGCTC 120

Qy 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
    |||
Db 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180

Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225

RESULT 2
LOCUS I36933 225 bp DNA PAT 13-MAY-1997
DEFINITION Sequence 18 from patent US 5612201.
ACCESSION I36933
VERSION I36933.1 GI:2084893
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 225)
AUTHORS De Plaen,E., Boon-Falleur,T., Lethe ,B., Szkora,J., De Smet,C. and
Chomez,P.
TITLE Isolated nucleic acid molecules useful in determining expression of
a tumor rejection antigen precursor
JOURNAL Patent: US 5612201-A 18 18-MAR-1997;
FEATURES
source 1..225
/organism="unknown"
BASE COUNT 44 a 65 c 58 g 58 t
ORIGIN

Query Match      100.0%; Score 225; DB 6; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.9e-43;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATC 60
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Db 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATC 60

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTTGGCACCTGCCTGGGCTC 120
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Qy 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
    |||
Db 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180

Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
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Db 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225

RESULT 3
LOCUS HSU10339 945 bp mRNA PRI 13-JUN-1994
DEFINITION Human MAGE-3b mRNA, complete cds.
ACCESSION U10339
VERSION U10339.1 GI:499121
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KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 945)
AUTHORS Fenton,R.G.
TITLE Cloning and Analysis of MAGE-1 Related Genes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 945)
AUTHORS Fenton,R.G.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-1994) Robert G. Fenton, BRMP, NCI-FCRDC,
Frederick, MD 21702, USA
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MAGE-3b"
/haplotype="HLA-A1/A2"
/cell_line="DM150"
/cell_type="melanoma"
/tissue_type="skin"
/clone_lib="DM150 library"
/dev_stage="adult"
/notes="cancer patient"
CDS
1..945
/codon_start=1
/product="MAGE-3b"
/protein_id="AAAI9006.1"
/db_xref="GI:499122"
/translation="MPLEQRSHQKPEEGLEARGEALGLVGAQAPATEEQEAASSST
LVEVTGLGEVPAESPPQSPQSGASLPTTMYNPLWSQSYEDSSNOEEGSPFPDLE
SEFQAALSRKVAKLHFLLLKYRAREPVTAKMGLSVGVNMOYFFPVIFSKASDSLQL
VFGEIEMVDPIGHVYIFATCLGSLDGLLDNQIMPKTGFLIIILAIIAKEGDCAPE
EKIWEELSVLEVEFEGREDSIFGDPKKLLTQYFVOENLYEYRQVFGSDPACYEFWGPFR
ALTIETSYKVLHMHVKISGGPRISYPLLHFWALREGEE"
BASE COUNT 213 a 254 c 275 g 203 t
ORIGIN

Query Match      97.9%; Score 220.2; DB 9; Length 945;
Best Local Similarity 98.7%; Pred. No. 2.2e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATC 60
    |||
Db 433 TACTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCCTTGCAGCTGGTCTTTGGCATC 492

Qy 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCTC 120
    |||
Db 493 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCTC 552

Qy 121 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 180
    |||
Db 553 TCCTACGATGCCCTGCTGGGTGACAATCAGATCATGCCCCAGGACAGGCTTCCTGATAATC 612

Qy 181 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 225
    |||
Db 613 ATCCTGGCCATAATCGCAAGAGAGGGCGACTGTGCCCTGAGGAG 657

RESULT 4
LOCUS HUMMAGEB 1019 bp mRNA PRI 07-FEB-1999
DEFINITION Human mRNA for MAGE-6 protein, complete cds.
ACCESSION D32076
VERSION D32076.1 GI:1125015
KEYWORDS MAGE-6 protein; melanoma antigen.
SOURCE Homo sapiens cell-line M73 cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE 1 (bases 1 to 1019)
AUTHORS Imai,Y.
TITLE Direct Submission
JOURNAL Submitted (08-JUL-1994) to the DDBJ/EMBL/GenBank Databases.
Yasuhisa Imai, Kurume University School of Medicine, Immunology;
Asahi 67, Kurume, Fukuoka 830, Japan (Tel:0942-31-7551,
Fax:0942-31-7699)
REFERENCE 2 (bases 1 to 1019)
AUTHORS Imai,Y., Shichijo,S., Yamada,A., Katayama,T., Yano,H. and Itoh,K.
TITLE Sequence analysis of the MAGE gene family encoding human
tumor-rejection antigens
JOURNAL Gene 160 (2), 287-290 (1995)
MEDLINE 95369706
FEATURES
source Location/Qualifiers
1..1019
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="M73"
66..1010
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/note="Nomenclature of MAGE-6 was according to MAGE gene's
27 nucleotide sequences of HLA-A1 binding motif (Traversari
etc., 1992)"
/codon_start=1
/evidence=experimental
/product="MAGE-6 protein"
/protein_id="BAA06842.1"
/db_xref="GI:1125016"
/translation="MPLRQSOHCKPEEGLEARGALGLVGAQAPATERQEAASST
LVEVLGVPAESDPQSPQASLPPTMNPWMSQSYEDSSNOEEGSPFFDLE
SEFQALSRKVAKLHVFLLKRYAREPVTAKMLGSVGNWQYFFPVPFSKASDSLQ
VEGIELMEYDIIYFATCLGLSDGLGDNQIMPKTFLIILAIKAGDCAPE
EKIWEISLVFEFGREDSIFGDPKLLTQVFOENYLEYRQVPGSDPACYEFLWGP
ALIEYSYKVLHMHVKISGPRISYPLLHWEALREGEE"
BASE COUNT 224 a 284 c 292 g 219 t
ORIGIN

Query Match 97.9%; Score 220.2; DB 9; Length 1019;
Best Local Similarity 98.7%; Pred. No. 2.2e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATC 60
|||
Db 498 TACTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATC 557
QY 61 GAGCTGATGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 120
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Db 558 GAGCTGATGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 617
QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACGAGCTTCCTGATAATC 180
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Db 618 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACGAGCTTCCTGATAATC 677
QY 181 ATCTTGCCCAATATCGCAAGAGGGCGACTGTGCCCTCGAGGAG 225
|||
Db 678 ATCTTGCCCAATATCGCAAGAGGGCGACTGTGCCCTCGAGGAG 722

RESULT 5
AX019384
LOCUS AX019384 1362 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 10 from Patent WO9940188.
ACCESSION AX019384
VERSION AX019384.1 GI:10043354
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1362)
AUTHORS Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
TITLE Tumor-associated antigen derivatives from the mage family, and

nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
Patent: WO 9940188-A 10 12-AUG-1999;
SLAOUI MONCEF MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
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/db_xref="taxon:9606"
/note="Melanoma tissue"
BASE COUNT 345 a 348 c 383 g 286 t
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Query Match 97.9%; Score 220.2; DB 6; Length 1362;
Best Local Similarity 98.7%; Pred. No. 2.1e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATC 60
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Db 823 TACTTCTTCTGTGATCTTCAGCAAGCTTCGATTCCTTCGAGCTGGTCTTTGGCATC 882
QY 61 GAGCTGATGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 120
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Db 883 GAGCTGATGAAGTGGACCCATCGCCAGCTGTACATCTTTGCCACCTGCCTGGGCCTC 942
QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACGAGCTTCCTGATAATC 180
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Db 943 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCAGGACGAGCTTCCTGATAATC 1002
QY 181 ATCTTGCCCAATATCGCAAGAGGGCGACTGTGCCCTCGAGGAG 225
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Db 1003 ATCTTGCCCAATATCGCAAGAGGGCGACTGTGCCCTCGAGGAG 1047

RESULT 6
HSU10691
LOCUS Human MAGE-6 antigen (MAGE6) gene, complete cds. 23-JUN-1995
DEFINITION
ACCESSION U10691
VERSION U10691.1 GI:533522
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3871)
AUTHORS De Plaen,E., Arden,K., Traversari,C., Gaforio,J.J., Szikora,J.P.,
De Smet,C., Brasseur,F., van der Bruggen,P., Lethe,B., Lurquin,C.,
Brasseur,R., Chomez,P., De Backer,O., Cavenee,W. and Boon,T.
TITLE Structure, chromosomal localization, and expression of 12 genes of
the MAGE family
JOURNAL Immunogenetics 40 (5), 360-369 (1994)
MEDLINE 95012457
REFERENCE 2 (bases 1 to 3871)
AUTHORS De Plaen,E.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1994) Etienne De Plaen, Ludwig Institute for
Cancer Research, 74 Avenue Hippocrate, Brussels, 1200, Belgium
Location/Qualifiers
1..3871
/organism="Homo sapiens"
/isolate="patient MZ2"
/db_xref="taxon:9606"
/chromosome="X"
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/tissue_type="blood"
/dev_stage="adult"
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/number=2
2199..23762
/number=3

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gene 2264..3208
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CDS 2264..3208
/gene="MAGE6"
/codon_start=1
/product="MAGE-6 antigen"
/protein_id="AAA68875.1"
/db_xref="GI:533523"
/translation="MPLEQRSQHGKPEEGLEARGALGLVGAQAPATEEEAASSST
LVEVTLGEVPAESPDPQSGASSLPPTMNYPLWQSYEDDSNOEEGPGSTPFDLE
SEFOALSRKVKLVHLLKLYRAREPVTKAEMLGSVGNWQVFPVLFKASDSLQ
VEGLEMEVDPIGHVYIFATCLGLSDGLLDNOIMPKTGFLLIILAIKAGDCAP
EKIWEELSLEVEFGREDSIFGDPKLLLTQFYQENILEYKQVPSDPACTYFLWGPR
ALISYTKVVLHMHVKISGGPRISYLIHLEWALREGEE"
BASE COUNT 865 a 1050 c 1117 g 839 t
ORIGIN

Query Match 97.9%; Score 220.2; DB 9; Length 3871;
Best Local Similarity 98.7%; Pred. No. 1.9e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCTTTCTGTGATCTTCAGCAAGCTCCGATTCCTTGCAGCTGCTTTTGGCATC 60
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Db 2686 TACTTCTTTCTGTGATCTTCAGCAAGCTCCGATTCCTTGCAGCTGCTTTTGGCATC 2755

QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCTC 120
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Db 2756 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCTC 2815

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|||
Db 2816 TCCTACGATGGCTCTCTGGGTGACAATCAGATCATGCCAGACAGAGCTTCTGTATAATC 2875

QY 181 ATCTGGCCATAATCGCAAGAGAGGCGACTGTGCCCTGAGGAG 225
|||
Db 2876 ATCTGGCCATAATCGCAAGAGAGGCGACTGTGCCCTGAGGAG 2920

RESULT 7
AF002997
LOCUS AF002997 245077 bp DNA PRI 13-APR-2001
DEFINITION Homo sapiens chromosome X map Xq28, complete sequence.
ACCESSION AF002997
VERSION AF002997.2 GI:13621226
KEYWORDS HTG; HTGS_ACTIVEFIN.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Gloeckner,G., Rosenthal,A., Drescher,B., Schattevoy,R., Poustka,A.
and Kioschis,P.
Genomic sequence in Xq28
Unpublished
REFERENCE 2 (bases 1 to 245077)
Galgoczy,P., Schillabel,M., Rosenthal,A. and Platzzer,M.
Chromosome X genomic sequence
Unpublished
REFERENCE 3 (bases 1 to 245077)
Gloeckner,G., Rosenthal,A., Drescher,B. and Schattevoy,R.
Direct Submission
JOURNAL Submitted (07-MAY-1997) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
REFERENCE 4 (bases 1 to 245077)
Platzzer,M.
Direct Submission
JOURNAL Submitted (13-APR-2001) Genome Analysis, Institute of Molecular
Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
COMMENT On Apr 13, 2001 this sequence version replaced gi:4409798.
FEATURES
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/organism="Homo sapiens"
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/chromosome="X"
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9444..45606
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/clone="CTD-2530F8"
/clone_lib="CalTech human BAC library D"
33939..72299
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="LO0630, cosmid"
42555..245077
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/clone="CTD-2507L14"
/clone_lib="CalTech human BAC library D"
BASE COUNT 70149 a 53336 c 52595 g 68996 t 1 others
ORIGIN

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Best Local Similarity 98.7%; Pred. No. 1.2e-42;
Matches 222; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TATTTCTTTCTGTGATCTTCAGCAAGCTCCGATTCCTTGCAGCTGCTTTTGGCATC 60
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QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCTC 120
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Db 164180 GAGCTGATGGAAGTGGACCCATCGCCACGCTGTACATCTTTGCCACCTGCTGGGCTC 164239

QY 121 TCCTACGATGGCTCTCTGGGTGACAATCAGATCATGCCAGACAGAGCTTCTGTATAATC 180
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Db 164240 TCCTACGATGGCTCTCTGGGTGACAATCAGATCATGCCAGACAGAGCTTCTGTATAATC 164299

QY 181 ATCTGGCCATAATCGCAAGAGAGGCGACTGTGCCCTGAGGAG 225
|||
Db 164300 ATCTGGCCATAATCGCAAGAGAGGCGACTGTGCCCTGAGGAG 164344

RESULT 8
AX019380
LOCUS AX019380 1212 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 6 from Patent WO9940188.
ACCESSION AX019380
VERSION AX019380.1 GI:10043352
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1212)
Slaoui,M.M., Cohen,J., Cabezon,S.T. and Vinals,B.C.
Tumor-associated antigen derivatives from the mage family, and
nucleic acid sequences encoding them, used for the preparation of
fusion proteins and of compositions for vaccination
Patent: WO 9940188-A 6 12-AUG-1999;
SLAOUT MONCFE MOHAMED (BE); SMITHKLINE BEECHAM BIOLOG (BE); COHEN
JOSEPH (BE); CABEZON SILVA TERESA (BE); VINALS BASSOLS CARLOTA (BE)
JOURNAL
Location/Qualifiers
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/organism="Homo sapiens"
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Db	994	GTCTGCGCCATAATCGCAAGAGAGGGCGGACTGTGCCCTGAGGAG	1038
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DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
Conservative			
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QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGGTCTTTGGCATC 60
Db 604 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGGTCTTTGGCATC 663
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Db 664 GAGCTGATGGAAGTGGACCCATCGCCACCTGACATCTTTGCCACCTGGCTGGGCCTC 723
QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTGTGATAATC 180
Db 724 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTGTGATAATC 783
QY 181 ATCTGGCCATAATCGCAGAGAGGGCGACTGTCGCCCTGAGGAG 225
Db 784 GTCTGGCCATAATCGCAGAGAGGGCGACTGTCGCCCTGAGGAG 828

RESULT 12
BC011744
LOCUS BC011744 1663 bp mRNA PRI 02-AUG-2001
DEFINITION Homo sapiens, Similar to melanoma antigen, family A, 3, clone
MGC:19667 IMAGE:3345801, mRNA, complete cds.
ACCESSION BC011744
VERSION BC011744.1 GI:15079897
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1663)
Strausberg, R.
Direct Submission
Submitted (30-JUL-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapps-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
cDNA Library Preparation: Ruben Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 27 Row: b Column: 12
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
FEATURES
Location/Qualifiers
1. 1663
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:19667 IMAGE:3345801"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
/note="vector: pOTB7"
145..1089
/codon_start=1
/product="Similar to melanoma antigen, family A, 3"

CDS
FEATURES
source
1. 1663
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:19667 IMAGE:3345801"
/tissue_type="Skin, melanotic melanoma."
/clone_lib="NIH_MGC_20"
/lab_host="DH10B-R"
/note="vector: pOTB7"
145..1089
/codon_start=1
/product="Similar to melanoma antigen, family A, 3"

Query Match 95.0%; Score 213.8; DB 9; Length 1663;
Best Local Similarity 96.9%; Pred. No. 6.7e-41;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGGTCTTTGGCATC 60
Db 577 TATTTCTTCTGTGATCTTCAGCAAGCTTCAGATTCTTCAGCTGGTCTTTGGCATC 636
QY 61 GAGCTGATGGAAGTGGACCCATCGCCACGCTGACATCTTTGCCACCTGGCTGGGCCTC 120
Db 637 GAGCTGATGGAAGTGGACCCATCGCCACCTGACATCTTTGCCACCTGGCTGGGCCTC 696
QY 121 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTGTGATAATC 180
Db 697 TCCTACGATGGCTGCTGGGTGACAATCAGATCATGCCCCAGCAGGCTTCTGTGATAATC 756
QY 181 ATCTGGCCATAATCGCAGAGAGGGCGACTGTCGCCCTGAGGAG 225
Db 757 GTCTGGCCATAATCGCAGAGAGGGCGACTGTCGCCCTGAGGAG 801

RESULT 13
BC000340
LOCUS BC000340 1709 bp mRNA PRI 12-JUL-2001
DEFINITION Homo sapiens, melanoma antigen, family A, 3, clone MGC:8564
IMAGE:2822978, mRNA, complete cds.
ACCESSION BC000340
VERSION BC000340.1 GI:12653144
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1709)
Strausberg, R.
Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapps-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ruben Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
```

Series: IRAL Plate: 1 Row: k Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7280331.

FEATURES

source

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1. .1709
/organism="Homo sapiens"
/db_xref="LocusID:4102"
/db_xref="taxon:9606"
/clone="MGC:8564 IMAGE:2822978"
/tissue_type="lung, small cell carcinoma"
/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
/notes="Vector: pORB7"
184. .1128
/codon_start=1
/product="melanoma antigen, family A, 3"
/protein_id="AAH0340.1"
/db_xref="GI:12653145"
/translation="MPLEORSQHCKPEEGLEARGEALGLVGAQAPATEEEQEAASSST
LVEVTIGVPAEASDPQSGQSLPTMNYPLWSQSYEDSSNOEEGSPFFDLE
SEFQAALSRKVAELVHLLKYRAREPVTKAEMLGSVGNWQYFFPVIFSKASSLQ
VEGIELMEVDPIGHLYIFATCLGLSYDGLGDNQIMPKAGLLIIVLAIAREGDCAPE
EKIWEELSVLEVFEGRESILGDPKLLTQHVFQENYLEYRQVPSDPAFYELWGP
ALVETSYVKLVHMHVKSIGGPHISYPPLHFWLREGE"
422 a 408 c 468 g 411 t
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BASE COUNT

ORIGIN

Query Match 95.0%; Score 213.8; DB 9; Length 1709;

Best Local Similarity 96.9%; Pred. No. 6.7e-41;

Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 1 TATTCTCTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCGAGCTGGTCTTTGGCATC 60
|||||
Db 616 TATTCTCTTCTGTGATCTTCAGCAAGCTTCAGTTCCTTGCGAGCTGGTCTTTGGCATC 675
|||||
QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCGCTC 120
|||||
Db 676 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCGCTC 735
|||||
QY 121 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGCGTTCCTGTGATAATC 180
|||||
Db 736 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGCGTTCCTGTGATAATC 795
|||||
QY 181 ATCTCGGCATATTCGCAAGAGGCGGACTGTGCCCTGAGGAG 225
|||||
Db 796 GTCTGGCCATATTCGCAAGAGGCGGACTGTGCCCTGAGGAG 840
|||||
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RESULT 14

BC005963

LOCUS

DEFINITION

IMAGE:4064879, melanoma antigen, family A, 3, clone MGC:14613

BC005963

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 1753)

Strausberg, R.

Direct Submission

Submitted (02-APR-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: CLONTECH Laboratories, Inc.

REMARK

COMMENT

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 21 Row: a Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.

FEATURES

source

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1. .1753
/organism="Homo sapiens"
/db_xref="LocusID:4102"
/db_xref="taxon:9606"
/clone="MGC:14613 IMAGE:4064879"
/tissue_type="Bone marrow, chronic myelogenous leukemia"
/clone_lib="NIH_MGC_54"
/lab_host="DH10B"
/notes="Vector: pDNR-LIB"
210. .1154
/codon_start=1
/product="melanoma antigen, family A, 3"
/protein_id="AAH05963.1"
/db_xref="GI:13543627"
/translation="MPLEORSQHCKPEEGLEARGEALGLVGAQAPATEEEQEAASSST
LVEVTIGVPAEASDPQSGQSLPTMNYPLWSQSYEDSSNOEEGSPFFDLE
SEFQAALSRKVAELVHLLKYRAREPVTKAEMLGSVGNWQYFFPVIFSKASSLQ
VEGIELMEVDPIGHLYIFATCLGLSYDGLGDNQIMPKAGLLIIVLAIAREGDCAPE
EKIWEELSVLEVFEGRESILGDPKLLTQHVFQENYLEYRQVPSDPAFYELWGP
ALVETSYVKLVHMHVKSIGGPHISYPPLHFWLREGE"
436 a 423 c 474 g 420 t
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BASE COUNT

ORIGIN

Query Match 95.0%; Score 213.8; DB 9; Length 1753;

Best Local Similarity 96.9%; Pred. No. 6.7e-41;

Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 1 TATTCTCTTCTGTGATCTTCAGCAAGCTTCGGATTCCTTGCGAGCTGGTCTTTGGCATC 60
|||||
Db 642 TATTCTCTTCTGTGATCTTCAGCAAGCTTCAGTTCCTTGCGAGCTGGTCTTTGGCATC 701
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QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCGCTC 120
|||||
Db 702 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCCTGGGCGCTC 761
|||||
QY 121 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGCGTTCCTGTGATAATC 180
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Db 762 TCCTAGATGGCTGCTGGGTGACATCAGATCATGCCAGGACAGCGTTCCTGTGATAATC 821
|||||
QY 181 ATCTCGGCATATTCGCAAGAGGCGGACTGTGCCCTGAGGAG 225
|||||
Db 822 GTCTGGCCATATTCGCAAGAGGCGGACTGTGCCCTGAGGAG 866
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RESULT 15

AR079453

LOCUS

DEFINITION

Sequence 1 from patent US 5965535.

AR079453

ACCESSION

VERSION

AR079453.1 GI:10006198

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

1 (bases 1 to 4204)

REFERENCE

AUTHORS

Chaux, P., Stroobant, V., Boon-Falleur, T. and van der Bruggen, P.

MAGE-3 peptides presented by HLA class II molecules

31-AUG-2000

DNA

PAT

JOURNAL Patent: US 5965535-A 1 12-OCT-1999;
FEATURES Location/Qualifiers
Source I. 4204
BASE COUNT 944 a 1144 c 1223 g 893 t
ORIGIN

Query Match 95.0%; Score 213.8; DB 6; Length 4204;
Best Local Similarity 96.9%; Pred. No. 6.1e-41;
Matches 218; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TATTTCTTTCCTGTGATCTTCAGCAAGCTTCCGATTCCCTGCAGCTGGTCTTTGGCATC 60
Db 2897 TATTTCTTTCCTGTGATCTTCAGCAAGCTTCCGATTCCCTGCAGCTGGTCTTTGGCATC 2956

QY 61 GAGCTGATGGAAGTGGACCCCATCGGCCACGTGTACATCTTTGCCACCTGCCTGGGCCTC 120
Db 2957 GAGCTGATGGAAGTGGACCCCATCGGCCACTTGTACATCTTTGCCACCTGCCTGGGCCTC 3016

QY 121 TCCTACGATGGCCTCTCGGTGACAATCAGATCATSCCCAGCAGCAGGCTTCTGTATAATC 180
Db 3017 TCCTACGATGGCCTCTCGGTGACAATCAGATCATSCCCAGCAGCAGGCTTCTGTATAATC 3076

QY 181 ATCCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 225
Db 3077 GTCTGGCCATAATCGCAAGAGAGGGGACTGTGCCCTGAGGAG 3121

Search completed: December 4, 2001, 12:17:04
Job time: 9082 sec